

GenCore version 5.1.7  
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OM nucleic - nucleic search, using sw model

Run on: March 17, 2006, 10:45:07 ; Search time 2012 Seconds  
(without alignments)  
6502.066 Million cell updates/sec

Title: US-10-649-193-14  
Perfect score: 1582  
Sequence: 1 CGAGCCGCGAGCGCCGCC.....gtctccccctgcagccgtg 1582

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications NA\_Main:\*

- 1: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq:\*
- 2: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq:\*
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- 10: /cgn2\_6/ptodata/1/pubpna/US11\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

RESULT 1  
US-09-191-724-14  
; Sequence 14, Application US/09191724  
; Patent No. US20020055617A1  
; GENERAL INFORMATION:  
; APPLICANT: Perrin, Marilyn H.  
; APPLICANT: Chen, Ruoping  
; APPLICANT: Lewis, Kathy A.  
; APPLICANT: Vale Jr., Wylie W.  
; APPLICANT: Donaldson, Cynthia J.  
; APPLICANT: Sawchenko, Paul  
; TITLE OF INVENTION: Cloning and Recombinant Production of  
; TITLE OF INVENTION: CRF Receptor(s)  
; FILE REFERENCE: Salk1748  
; CURRENT APPLICATION NUMBER: US/09/191,724  
; CURRENT FILING DATE: 1998-11-12  
; EARLIER APPLICATION NUMBER: US 08/374,009  
; EARLIER FILING DATE: 1995-01-17  
; EARLIER APPLICATION NUMBER: US 08/353,537  
; EARLIER FILING DATE: 1994-12-09  
; EARLIER APPLICATION NUMBER: PCT/US94/05908  
; EARLIER FILING DATE: 1993-05-25  
; EARLIER APPLICATION NUMBER: US 08/110,286  
; EARLIER FILING DATE: 1993-08-23  
; EARLIER APPLICATION NUMBER: US 08/079,320  
; EARLIER FILING DATE: 1993-06-18  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 14  
; LENGTH: 1582  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (82)...(1413)  
; OTHER INFORMATION: CRF-R splice-variant insert fragment inserted  
; OTHER INFORMATION: between nucleotides 516-517 of SEQ ID NO:1.  
; OTHER INFORMATION: /note= "This sequence is contained in clone  
; OTHER INFORMATION: "CRF-R2".  
US-09-191-724-14

Query Match 100.0%; Score 1582; DB 3; Length 1582;  
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Matches 1582; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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## RESULT 2

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US-10-649-193-14
; Sequence 14, Application US/10649193
; Publication No. US20040039173A1
; GENERAL INFORMATION:
; APPLICANT: Perrin, Marilyn H.
; APPLICANT: Chen, Ruoping
; APPLICANT: Lewis, Kathy A.
; APPLICANT: Vale Jr., Wylie W.
; APPLICANT: Donaldson, Cynthia J.
; APPLICANT: Sawchenko, Paul
; TITLE OF INVENTION: Cloning and Recombinant Production of
; FILE REFERENCE: Salk1748
; CURRENT APPLICATION NUMBER: US/10/649,193
; PRIOR FILING DATE: 2003-08-26
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/191,724
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-12
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 08/374,009
; PRIOR FILING DATE: EARLIER FILING DATE: 1995-01-17
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 08/353,537
; PRIOR FILING DATE: EARLIER FILING DATE: 1994-12-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: PCT/US94/05908
; PRIOR FILING DATE: EARLIER FILING DATE: 1993-05-25
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 08/110,286
; PRIOR FILING DATE: EARLIER FILING DATE: 1993-08-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 08/079,320
; PRIOR FILING DATE: EARLIER FILING DATE: 1993-06-18
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 14
; LENGTH: 1582
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (82)...(1413)
; OTHER INFORMATION: CRF-R splice-variant insert fragment inserted
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/ SEQ ID NO 1
/ LENGTH: 1495
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (82)...(1326)
/ OTHER INFORMATION: /product = "Human pituitary CRF-receptor"
/ OTHER INFORMATION: /note= "This sequence is encoded by clone
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US-09-191-724-1

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Matches 1495; Conservative 0; Mismatches 0; Indels 87; Gaps 1;

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## RESULT 4

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US-10-649-193-1
; Sequence 1, Application US/10649193
; Publication No. US20040039173A1
; GENERAL INFORMATION:
; APPLICANT: Perrin, Marilyn H.
; APPLICANT: Chen, Ruoping
; APPLICANT: Lewis, Kathy A.
; APPLICANT: Vale Jr., Wylie W.
; APPLICANT: Donaldson, Cynthia J.
; APPLICANT: Sawchenko, Paul
; TITLE OF INVENTION: Cloning and Recombinant Production of
; FILE REFERENCE: Salk1748
; CURRENT FILING DATE: 2003-08-26
; PRIOR APPLICATION NUMBER: US/10/649,193
; PRIOR FILING DATE: 1998-11-12
; PRIOR APPLICATION NUMBER: US 08/374,009
; PRIOR FILING DATE: 1995-01-17
; PRIOR APPLICATION NUMBER: US 08/353,537
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APPLICANT: Gulukota, Kamalakara  
APPLICANT: Graham, James R.  
TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL SECRETED PROTEINS  
FILE REFERENCE: GIN 6402  
CURRENT APPLICATION NUMBER: US/09/822,830A  
CURRENT FILING DATE: 2001-03-29  
PRIOR APPLICATION NUMBER: 60/195,604  
PRIOR FILING DATE: 2000-04-06  
NUMBER OF SEQ ID NOS: 631  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 30  
LENGTH: 2579  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-822-830A-30

Query Match 88.4%; Score 1398; DB 3; Length 2579;  
Best Local Similarity 94.5%; Pred. No. 0;  
Matches 1495; Conservative 0; Mismatches 0; Indels 87; Gaps 1;

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2420 CGAGCCGCGAGCGCCGCGGCTCTCTGGGATGTCCTAGGACCGGGCATTCAGGAC 2361  
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2360 GGTAGCCGAGCGAGCGCGGATGGGAGGACCCGCGAGCTCCGCTCTCGTCAAGGCCCTT 2301  
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1907 ----- 1908  
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1727 TGGATGTTCCGCGAGGCTGTACCTGCACACAGCCATGTGTCACTCACTCACTGAC 1668  
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1667 CGGCTCGGCAAAATGGATGTTTCATCTGCTGGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1608  
901 GCTGGGCAATGGGAGGCTGTACTACGACAAATGAGAAGTGTGGTTTGGCAAAAGGCT 960  
1607 GCTGGGCAATGGGAGGCTGTACTACGACAAATGAGAAGTGTGGTTTGGCAAAAGGCT 1548  
961 GGGGTGTACACCGACTACATCTACAGGGCCCATCATCTCTGCTCTGCTGATCAATTC 1020  
1547 GGGGTGTACACCGACTACATCTACAGGGCCCATCATCTCTGCTCTGCTGATCAATTC 1488  
1021 ATCTTCTTTTCAACATCTGCTGCGCATCTCATGACCAAGCTCCGGGCATCCACAGCTCT 1080  
1487 ATCTTCTTTTCAACATCTGCTGCGCATCTCATGACCAAGCTCCGGGCATCCACAGCTCT 1428  
1081 GAGACCATTCAGTACAGGAGGCTGTGAAGCCACTCTCTGCTGCTGCTGCTGCTGCTGCTGCT 1140  
1427 GAGACCATTCAGTACAGGAGGCTGTGAAGCCACTCTCTGCTGCTGCTGCTGCTGCTGCTGCT 1368  
1141 ATCACTTACATGCTGTTCTTCTGTCATCCCGGGAGGATGAGGTCTCCCGGGTCTGCTTTC 1200  
1367 ATCACTTACATGCTGTTCTTCTGTCATCCCGGGAGGATGAGGTCTCCCGGGTCTGCTTTC 1308  
1201 ATCTACTTCAACTCTCTTCTGGAATCTCTTCAAGGCTTCTTGTGTGTGTGTGTGTGTGTGT 1260  
1307 ATCTACTTCAACTCTCTTCTGGAATCTCTTCAAGGCTTCTTGTGTGTGTGTGTGTGTGTGT 1248  
1261 TTCTTCAATAGTGTGCTCGTTCTGTCATCCGGAAGGTTGACCGGTGGCAGGACAAG 1320  
1247 TTCTTCAATAGTGTGCTCGTTCTGTCATCCGGAAGGTTGACCGGTGGCAGGACAAG 1188  
1321 CACTCGATCCGTGCCCGAGTGGCCGTCATGTCATCCCACTCCCACTCCCACTCCCACTCCG 1380  
1187 CACTCGATCCGTGCCCGAGTGGCCGTCATGTCATCCCACTCCCACTCCCACTCCCACTCCG 1128  
1381 AGTTTTCACAGCATCAAGCAGTCCACAGAGTCTGAGCTGGGAGGATGAGTGGAGGAGGAGG 1440  
1127 AGTTTTCACAGCATCAAGCAGTCCACAGAGTCTGAGCTGGGAGGATGAGTGGAGGAGGAG 1068  
1441 CAAAGAGTGTGGTGGGGGATGACGGCAGGCTCCCTGACCCCTGCTGCTGCTGCTGCTGCTG 1500  
1067 CAAAGAGTGTGGTGGGGGATGACGGCAGGCTCCCTGACCCCTGCTGCTGCTGCTGCTGCTG 1008  
1501 GACCTGTAGGTCTCATGCCACTCCCGCAGGAGCAGCTGGCACTGACAGCCTGGGGGGG 1560  
1007 GACCTGTAGGTCTCATGCCACTCCCGCAGGAGCAGCTGGCACTGACAGCCTGGGGGGG 948  
1561 CGCTCTCCCTCCGAGCCGTG 1582  
947 CGCTCTCCCTCCGAGCCGTG 926

RESULT 6  
US-09-799-978-1  
; Sequence 1, Application US/09799978  
; Publication No. US20030165807A1  
; GENERAL INFORMATION:  
; APPLICANT: The Procter & Gamble Company  
; APPLICANT: Isfort, Robert  
; APPLICANT: Sheldon, Russell  
; TITLE OF INVENTION: Methods for Identifying Compounds for Regulating Muscle Mass or  
; TITLE OF INVENTION: Function Using Corticotropin Releasing Factor Receptors  
; FILE REFERENCE: 8448  
; CURRENT APPLICATION NUMBER: US/09/799,978  
; CURRENT FILING DATE: 2001-03-06  
; NUMBER OF SEQ ID NOS: 44  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 1  
; LENGTH: 2536



Query Match 88.3%; Score 1396.4; DB 7; Length 2536;  
Best Local Similarity 94.4%; Pred. No. 0;  
Matches 1494; Conservative 0; Mismatches 1; Indels 87; Gaps 1;  
QY 1 CGAGCCGCGAGCCGCGCGCGTCTCTGGAGATGCTCGTAGGACCCGGGCAATTCAGGAC 60  
DB 146 CGAGCCGCGAGCCGCGCGCGTCTCTGGAGATGCTCGTAGGACCCGGGCAATTCAGGAC 205  
QY 61 GGTAGCCGAGCGAGCCGCGAGGATGGAGGACCCCGCAGCTCCGTCTCGTCAAGGCCCTT 120  
DB 206 GGTAGCCGAGCGAGCCGCGAGGATGGAGGACCCCGCAGCTCCGTCTCGTCAAGGCCCTT 265  
QY 121 CTCCTTCTGGGGCTGAACCCCGTCTCTGCTCCCTCCAGACACGACTCCGAGAGCCTG 180  
DB 266 CTCCTTCTGGGGCTGAACCCCGTCTCTGCTCCCTCCAGACACGACTCCGAGAGCCTG 325  
QY 181 TCCTTGCGCAGCAATCTCAGACTGCAAGTCAAGCATCCGTGACCTCATTTGGCAAC 240  
DB 326 TCCTTGCGCAGCAATCTCAGACTGCAAGTCAAGCATCCGTGACCTCATTTGGCAAC 385  
QY 241 TGGTGGCCCGAGCCCTGGGGGCGAGTGTGTTGGCCCTGCCCTGCTTTTCTAT 300  
DB 386 TGGTGGCCCGAGCCCTGGGGGCGAGTGTGTTGGCCCTGCCCTGCTTTTCTAT 445  
QY 301 GGTGTCCGCTACAAATACCAAAATGGCTACCGGGAGTGCCTGGCCAAATGGCAGCTGG 360  
DB 446 GGTGTCCGCTACAAATACCAAAATGGCTACCGGGAGTGCCTGGCCAAATGGCAGCTGG 505  
QY 361 GCGCCGCGGTGAATTAATCCGAGTGCAGAGATCTCTCAATGAGGAGAAAAAAGCAAG 420  
DB 506 GCGCCGCGGTGAATTAATCCGAGTGCAGAGATCTCTCAATGAGGAGAAAAAAGCAAG 565  
QY 421 GTGCACATACATCTGCGAGTCAATCACTACTGGGCCACTGTATCTCCCTGGTGGCC 480  
DB 566 GTGCACATACATCTGCGAGTCAATCACTACTGGGCCACTGTATCTCCCTGGTGGCC 625  
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DB 626 CTCCTGGTGGCTTTGTCTCTTCTGCGGCTC----- 658  
QY 541 CAGGCGAGATGGAGCCCTGGAGGTGGGGGTCTCATGAGTGGTCCCAATTTCAAGTTGGA 600  
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QY 601 AGGAGCATCCGCTCGAABACATCATCCACTGGAACTCATCTCCGCTTCATCCCTG 660  
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QY 661 CGCAACGCCACCTGGTTCGTTGCTCCAGCTAAACATGAGCCCGAGGTCCACACAGAGCAAC 720  
DB 719 CGCAACGCCACCTGGTTCGTTGCTCCAGCTAAACATGAGCCCGAGGTCCACACAGAGCAAC 778  
QY 721 GTGGGCTGTTGAGTGTGAGCAGCGGCTTAACTACTTCCATGTGACCAACTTCTTC 780  
DB 779 GTGGGCTGTTGAGTGTGAGCAGCGGCTTAACTACTTCCATGTGACCAACTTCTTC 838  
QY 781 TGGATGTTGGCGAGGCTGTACTCTGCAACAGCCATCGTCTCACTTACTTCACTGAC 840  
DB 839 TGGATGTTGGCGAGGCTGTACTCTGCAACAGCCATCGTCTCACTTACTTCACTGAC 898  
QY 841 CGGCTCGCAAAATGGATGTTTCATCTGATGGCTGGGGTGTGCCCTTCCCCATCATTTGTG 900  
DB 899 CGGCTCGCAAAATGGATGTTTCATCTGATTTGGCTGGGGTGTGCCCTTCCCCATCATTTGTG 958  
QY 901 GCTTGGGCCATTGGGAAGCTGTACTAGCAATGAGAGTGTGGTTGGCAAAAGGCTT 960  
DB 959 GCTTGGGCCATTGGGAAGCTGTACTAGCAATGAGAGTGTGGTTGGCAAAAGGCTT 1018  
QY 961 GGGGTGTACACGACTACATCTACCGGGGCCCATGATCTCTGCTCTGCTGATCAATTC 1020  
DB 1019 GGGGTGTACACGACTACATCTACCGGGGCCCATGATCTCTGCTCTGCTGATCAATTC 1078  
QY 1021 ATCTTCTTTTCAACATCGTCCGATCTCTATGACCAAGCTCCGGGATCCACCAAGTCT 1080

DB 1079 ATCTTCTTTTCAACATCGTCCGATCTCTCATGACCAAGTCCGGGATCCACCAAGTCT 1138  
QY 1081 GAGACCATTCAGTACAGGAAGGCTGTGAAAGCCACTCTCTGGTGTCTGCTCCCTCTCTGGGC 1140  
DB 1139 GAGACCATTCAGTACAGGAAGGCTGTGAAAGCCACTCTCTGGTGTCTGCTCCCTCTCTGGGC 1198  
QY 1141 ATCACCCTACATGCTGTCTTCTGTCATCCCGGGAGATGAGGTCTCCCGGGTCTCTTC 1200  
DB 1199 ATCACCCTACATGCTGTCTTCTGTCATCCCGGGAGATGAGGTCTCCCGGGTCTCTTC 1258  
QY 1201 ATCTACTTCAACTCTCTTCTGGAATCTTCCAGGGCTTCTTGTGTCTGTGTCTACTGT 1260  
DB 1259 ATCTACTTCAACTCTCTTCTGGAATCTTCCAGGGCTTCTTGTGTCTGTGTCTACTGT 1318  
QY 1261 TTCTCTCAATAGTAGAGTCCGTTCTGCCATCCGGAAGAGTGGCACCGGTGGCAGGACAAG 1320  
DB 1319 TTCTCTCAATAGTAGAGTCCGTTCTGCCATCCGGAAGAGTGGCACCGGTGGCAGGACAAG 1378  
QY 1321 CACTCGATCCGTGCCGAGTGGCCGTGTCATGTCATCCCACTCCCACTCCCACTCCCACTCC 1380  
DB 1379 CACTCGATCCGTGCCGAGTGGCCGTGTCATGTCATCCCACTCCCACTCCCACTCCCACTCC 1438  
QY 1381 AGCTTTTCAAGCATCAAGCAGTCCACAGCAGTCTGAGCTGGCAGGTCTATGGAGCAGCCCC 1440  
DB 1439 AGCTTTTCAAGCATCAAGCAGTCCACAGCAGTCTGAGCTGGCAGGTCTATGGAGCAGCCCC 1498  
QY 1441 CAAAGAGCTGTGGCTGGGGGATGACGGCCAGGCTCCCTGACCACTGCTGTGGAGGT 1500  
DB 1499 CAAAGAGCTGTGGCTGGGGGATGACGGCCAGGCTCCCTGACCACTGCTGTGGAGGT 1558  
QY 1501 GACCTGTGAGTCTCATGCCCCTCCAGGAGCAGCTGGCAGCTGACAGCCTGGGGGGG 1560  
DB 1559 GACCTGTGAGTCTCATGCCCCTCCAGGAGCAGCTGGCAGCTGACAGCCTGGGGGGG 1618  
QY 1561 CCGCTCTCCCTTGCAGCCGTG 1582  
DB 1619 CCGCTCTCCCTTGCAGCCGTG 1640  
RESULT 8  
US-10-305-720-1360  
; Sequence 1360, Application US/10305720  
; Publication No. US20040010136A1  
; GENERAL INFORMATION:  
; APPLICANT: Au-Young, Janice K.; Seilhamer, Jeffrey J.  
; TITLE OF INVENTION: Composition for the Detection of Signaling Pathway Gene Expression  
; FILE REFERENCE: PA-0002-1 CON  
; CURRENT APPLICATION NUMBER: US/10/305,720  
; PRIOR FILING DATE: 2002-11-26  
; PRIOR APPLICATION NUMBER: 09/016,434  
; PRIOR FILING DATE: 1998-01-30  
; NUMBER OF SEQ ID NOS: 1490  
; SOFTWARE: PERL Program  
; SEQ ID NO 1360  
; LENGTH: 1335  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; OTHER INFORMATION: GenBank ID No. US20040010136A1 g408691  
US-10-305-720-1360  
Query Match 84.4%; Score 1335; DB 6; Length 1335;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 82 ATGGGAGGGCACCCGAGCTCCGCTCTCGTCAAGGCCCTTCTCTCTGCGGCTGAACCCC 141  
DB 1 ATGGGAGGGCACCCGAGCTCCGCTCTCGTCAAGGCCCTTCTCTCTGCGGCTGAACCCC 60  
QY 142 GTCTCTGCTCCCTCCAGGACAGCACTCGGAGAGCTCTCCCTGGCCAGCAACTCTCA 201

Db 61 GTCTCTGCTCCCTCAGGACAGCACTGCGAGGCTGTCCCTGGCCAGCAACATCTCA 120  
Qy 202 GGAAGTGGAGTGAACGATCCGTTGGACCTCATTTGGACCTGCTGGCCCGCCGAGCTGGG 261  
Db 121 GGAAGTGGAGTGAACGATCCGTTGGACCTCATTTGGACCTGCTGGCCCGCCGAGCTGGG 180  
Qy 262 GGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAG 321  
Db 181 GGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAG 240  
Qy 322 AACATGGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAG 381  
Db 241 AACATGGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAG 300  
Qy 382 GAGTGGAGAGATCTCAATGAG 441  
Db 301 GAGTGGAGAGATCTCAATGAG 360  
Qy 442 ATCATCAACTACCTGGGCACTGTATCTCCCTGGTGGCCCTCTGGTGGCCCTTGTGCTTC 501  
Db 361 ATCATCAACTACCTGGGCACTGTATCTCCCTGGTGGCCCTCTGGTGGCCCTTGTGCTTC 420  
Qy 502 TTTCTGGGCTCAGGCGAGGCTGACCCATTTGGGTTGACAGGAGATGAGGAGGAGGAGGAG 561  
Db 421 TTTCTGGGCTCAGGCGAGGCTGACCCATTTGGGTTGACAGGAGATGAGGAGGAGGAGGAG 480  
Qy 562 GTGGGGCTCAGTGGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 621  
Db 481 GTGGGGCTCAGTGGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 540  
Qy 622 AACATCACTGAGAGCTCATCTGGGCTTATCTGGGCAAGCCAGCTGGTGGTGGTGGTGG 681  
Db 541 AACATCACTGAGAGCTCATCTGGGCTTATCTGGGCAAGCCAGCTGGTGGTGGTGGTGGTGG 600  
Qy 682 GTCCAGCTAACATGAGCCCGAGGCTCCACAGAGCAAGCTGGGCTGGTGGTGGTGGTGGTGG 741  
Db 601 GTCCAGCTAACATGAGCCCGAGGCTCCACAGAGCAAGCTGGGCTGGTGGTGGTGGTGGTGG 660  
Qy 742 ACAGCCGCTACAACTACTTCCATGTGACCAACTTCTTGGATGTTGGCGAGGCTGC 801  
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Qy 802 TACTGGACAGAGCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 861  
Db 721 TACTGGACAGAGCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780  
Qy 862 ATCTGATTTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGG 921  
Db 781 ATCTGATTTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGG 840  
Qy 922 TACTGACAAATGAGAGTGTCTGTTTGGCAAGGCTGGGCTGTATACCGACTATATC 981  
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Qy 982 TACAGGGCCCCATGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1041  
Db 901 TACAGGGCCCCATGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960  
Qy 1042 CGCATCTCATGACCAAGCTCCGGGATCCACAGCTGAGACCAATTCAGTACAGGAAG 1101  
Db 961 CGCATCTCATGACCAAGCTCCGGGATCCACAGCTGAGACCAATTCAGTACAGGAAG 1020  
Qy 1102 GCTGTGAAAGCCACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1161  
Db 1021 GCTGTGAAAGCCACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1080  
Qy 1162 GTCAATCCCGGGAGGATGAGGCTCCCGGGTGTCTTCAATCTTCAATCTTCAATCTTCAATCTT 1221  
Db 1081 GTCAATCCCGGGAGGATGAGGCTCCCGGGTGTCTTCAATCTTCAATCTTCAATCTTCAATCTT 1140  
Qy 1222 GAATCTCTCAGGGCTCTTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1281  
Db 1141 GAATCTCTCAGGGCTCTTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1200

Qy 1282 TCTGCCATCCGAGAGGTGGCAACCGGTGGCAGGACAAGCACTCGATCCGTGCCGAGTG 1341  
Db 1201 TCTGCCATCCGAGAGGTGGCAACCGGTGGCAGGACAAGCACTCGATCCGTGCCGAGTG 1260  
Qy 1342 GCCCGTGGCATGTCCATCCCACTCCCAACCCGCTGTGAGCTTTTCCAGCATCAAGCAG 1401  
Db 1261 GCCCGTGGCATGTCCATCCCACTCCCAACCCGCTGTGAGCTTTTCCAGCATCAAGCAG 1320  
Qy 1402 TCCACAGCAGTCTGA 1416  
Db 1321 TCCACAGCAGTCTGA 1335

RESULT 9  
US-09-799-978-3  
; Sequence 3, Application US/09799978  
; Publication No. US20030165807A1  
; GENERAL INFORMATION:  
; APPLICANT: The Procter & Gamble Company  
; APPLICANT: Isfort, Robert  
; APPLICANT: Sheldon, Russell  
; TITLE OF INVENTION: Methods for Identifying Compounds for Regulating Muscle Mass or  
; TITLE OF INVENTION: Function Using Corticotropin Releasing Factor Receptors  
; FILE REFERENCE: 8448  
; CURRENT APPLICATION NUMBER: US/09/799,978  
; CURRENT FILING DATE: 2001-03-06  
; NUMBER OF SEQ ID NOS: 44  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 3  
; LENGTH: 1285  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (38)..(1285)  
US-09-799-978-3

Query Match 75.1%; Score 1188; DB 3; Length 1285;  
Best Local Similarity 93.7%; Pred. No. 0;  
Matches 1285; Conservative 0; Mismatches 0; Indels 87; Gaps 1;  
Qy 45 CCGGGCATTCAGGAGCGGTAGCCGAGGAGCCCGAGGATGGGAGGACCCCGAGCTCCG 104  
Db 1 CCGGGCATTCAGGAGCGGTAGCCGAGGAGCCCGAGGATGGGAGGACCCCGAGCTCCG 60  
Qy 105 TCTCGTCAAGGCCCTTCTCTTCTGGGGCTGAAACCCCGTCTCTGCTCTCCCTCCAGGACCA 164  
Db 61 TCTCGTCAAGGCCCTTCTCTTCTGGGGCTGAAACCCCGTCTCTGCTCTCCCTCCAGGACCA 120  
Qy 165 GCATCGAGAGCCTGTCTCTGGCCAGCAACATCTCAGGACTGAGTGCAGCATCCGT 224  
Db 121 GCATCGAGAGCCTGTCTCTGGCCAGCAACATCTCAGGACTGAGTGCAGCATCCGT 180  
Qy 225 GGAACCTCATTTGGACCTGTCTGGCCCGCCAGCCCTTGGGGCAGCTAGTGGTGGCCCTG 284  
Db 181 GGAACCTCATTTGGACCTGTCTGGCCCGCCAGCCCTTGGGGCAGCTAGTGGTGGCCCTG 240  
Qy 285 CCCTGCTTTTCTATGTTCTCGCTTACATAACAAATGAGTGTACCGGAGTGCCT 344  
Db 241 CCCTGCTTTTCTATGTTCTCGCTTACATAACAAATGAGTGTACCGGAGTGCCT 300  
Qy 345 GGCAATGGCAGTGGGCGCCCGCTGAAATTAATCCAGTGCAGGAGATCTCAATGA 404  
Db 301 GGCAATGGCAGTGGGCGCCCGCTGAAATTAATCCAGTGCAGGAGATCTCAATGA 360  
Qy 405 GGAAGAAAAAGCAAGTGCACCTACCATGTCGAGTGCATCACTACCTGGGCCATG 464  
Db 361 GGAAGAAAAAGCAAGTGCACCTACCATGTCGAGTGCATCACTACCTGGGCCATG 420  
Qy 465 TATCTCCCTGGTGGCCCTCTCTGTTGGCTTGTCTCTTCTGCGGCTCAGGCGAGGCTG 524  
Db 421 TATCTCCCTGGTGGCCCTCTCTGTTGGCTTGTCTCTTCTGCGGCTC----- 469

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QY 525 CACCCATTGGGTGACACGAGCAGATGGAGCCCTGGAGGTGGGGCTCCATGGAGTGGTGC 584
Db 470 ----- 469
QY 585 CCCATTTAGGTTGGAAGGAGCATCGGTGCTCGGAACATCATCCATCGGAACCTCAT 644
Db 470 -----AGGAGCATCCGGTGCCTGGGAACATCATCCATCGGAACCTCAT 513
QY 645 CTCGGCTTCATCTGCGGAAACGCACTCGGTGCTGGGTGCTGAGTAAACATAGAGCCCGA 704
Db 514 CTCGGCTTCATCTGCGGAAACGCACTCGGTGCTGGGTGCTGAGTAAACATAGAGCCCGA 573
QY 705 GGTCCACACGAGCAACGTGGGCTGCTGAGTGGGTGAGACGCGCTTACAACTACTTTCCA 764
Db 574 GGTCCACACGAGCAACGTGGGCTGCTGAGTGGGTGAGACGCGCTTACAACTACTTTCCA 633
QY 765 TGTGACCAACTCTTCTTGATGTTTCGCGAGGCTGCTACCTGCACACAGCCATCGTGT 824
Db 634 TGTGACCAACTCTTCTTGATGTTTCGCGAGGCTGCTACCTGCACACAGCCATCGTGT 693
QY 825 CACTACTCACTGACCGGCTGGGCAATGGATGTTTCATCTGATTTGGCTGGGGTGTGC 884
Db 694 CACTACTCACTGACCGGCTGGGCAATGGATGTTTCATCTGATTTGGCTGGGGTGTGC 753
QY 885 CTTCCCATCATTTGTCGCTGGGCAATGGATGTTTCATCTGATTTGGCTGGGGTGTGC 944
Db 754 CTTCCCATCATTTGTCGCTGGGCAATGGATGTTTCATCTGATTTGGCTGGGGTGTGC 813
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QY 1005 CTTGCTGATCAATTTCTTTCTTTTCAACATCGTCCGATCTCATGACCAAGCTCCG 1064
Db 874 CTTGCTGATCAATTTCTTTCTTTTCAACATCGTCCGATCTCATGACCAAGCTCCG 933
QY 1065 GGCATCCACACGCTGAGACCACTCAGTACAGGAAGGCTGCAAGGCCACTCTGGTGT 1124
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QY 1185 CTCGGGCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1244
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QY 1305 CCGGTGGCAGGCAAGCACTCGATCCGTCGCGGAGGCTGCGGATGTCATCCCTCCAC 1364
Db 1174 CCGGTGGCAGGCAAGCACTCGATCCGTCGCGGAGGCTGCGGATGTCATCCCTCCAC 1233
QY 1365 CTCGCCAACCCGTGTCAGTTTCAAGCATCAAGCATCAAGCATCAAGCATCAAGCATCAAG 1416
Db 1234 CTCGCCAACCCGTGTCAGTTTCAAGCATCAAGCATCAAGCATCAAGCATCAAGCATCAAG 1285

RESULT 10
US-10-649-852-3
; Sequence 3, Application US/10649852
; Publication No. US200401019111
; GENERAL INFORMATION:
; APPLICANT: The Procter & Gamble Company
; APPLICANT: Isfort, Robert
; APPLICANT: Sheldon, Russell
; TITLE OF INVENTION: Methods for Identifying Compounds for Regulating Muscle Mass or F
; TITLE OF INVENTION: Using Corticotropin Releasing Factor Receptors
; FILE REFERENCE: 8448R
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; CURRENT APPLICATION NUMBER: US/10/649,852
; CURRENT FILING DATE: 2003-08-27
; PRIOR APPLICATION NUMBER: US 09/799,978
; PRIOR FILING DATE: 2001-03-06
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 1285
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (38)..(1285)
; US-10-649-852-3

Query Match 75.1%; Score 1188; DB 7; Length 1285;
Best Local Similarity 93.7%; Pred. No. 0;
Matches 1285; Conservative 0; Mismatches 0; Indels 87; Gaps 1;

QY 45 CCGGGCATTTAGGACGGTAGCGAGCGAGCCCGAGGATGGGAGGCGACCCGCGAGCTCG 104
Db 1 CCGGGCATTTAGGACGGTAGCGAGCGAGCCCGAGGATGGGAGGCGACCCGCGAGCTCG 60
QY 105 TCTCGTCAAGGCCCTTCTCTCTCTGCGGTGAACCCCGTCTCTGCTCTCTCTCTCTCT 164
Db 61 TCTCGTCAAGGCCCTTCTCTCTCTGCGGTGAACCCCGTCTCTGCTCTCTCTCTCTCT 120
QY 165 GCATGCGAGAGCTGTCTCTGCGCAAGCAATCTCAGGACTGCGATGCAAGCATCCGT 224
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QY 225 GGACCTCATTTGGACCTGTCTGCGCCGCGAGCCCTGCGGGGAGCTAGTGTTCGGCCCTG 284
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QY 285 CCCTGCTTTTCTATGTTGTCCTGCTACAAATACCAAAACAATGGCTACCGGGAGTGCCT 344
Db 241 CCCTGCTTTTCTATGTTGTCCTGCTACAAATACCAAAACAATGGCTACCGGGAGTGCCT 300
QY 345 GGCCTAATGCGAGCTGGGCGCGCGGTGAATTTACTCCGAGTCCGAGGAGATCTCAATGA 404
Db 301 GGCCTAATGCGAGCTGGGCGCGCGGTGAATTTACTCCGAGTCCGAGGAGATCTCAATGA 360
QY 405 GAGGAAAAAAGCAAGGTGCACTACCATGTCGCGAGTCAATCACTACCTGCGGCACATG 464
Db 361 GAGGAAAAAAGCAAGGTGCACTACCATGTCGCGAGTCAATCACTACCTGCGGCACATG 420
QY 465 TATCTCCCTGTTGGCCCTCTCTGTTGGCTTTGTTCTCTTCTGCGGCTCAGGCGGCTG 524
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QY 525 CACCCATTTGGGTGACAGGCGAGATGGAGCCCTGGAGGTGGGGGCTCCATGGAGTGGTGC 584
Db 470 ----- 469
QY 585 CCCATTTAGGTTGGAAGGAGCATCGGTGCTCGGAACATCATCCATCGGAACCTCAT 644
Db 470 -----AGGAGCATCCGGTGCCTGGGAACATCATCCATCGGAACCTCAT 513
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Db 634 TGTGACCAACTCTTCTTGATGTTTCGCGAGGCTGCTACCTGCACACAGCCATCGTGT 693
QY 825 CACTACTCACTGACCGGCTGGGCAATGGATGTTTCATCTGATTTGGCTGGGGTGTGC 884
Db 694 CACTACTCACTGACCGGCTGGGCAATGGATGTTTCATCTGATTTGGCTGGGGTGTGC 884
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Db 694 CACCTACTCACTGACCGGCTGGCAAAATGATGTTTCACTGCTATGCTGGCTGGGGTGTGCC 753  
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Db 754 CTTTCCCATCATTTGTGGCCCTGGCCCAATGGGAAGCTGTACTACGACAATAGAAAGTGTG 813  
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Qy 1005 CTTGCTGATCAATTTTCACTTTCTTTTCAACATCGTCCGATCCTCATGACCAAGTCCG 1064  
Db 874 CTTGCTGATCAATTTTCACTTTCTTTTCAACATCGTCCGATCCTCATGACCAAGTCCG 933  
Qy 1065 GGCATCACCACTGTGAGACCAATTCAGTACAGGAAGGCTGTGAAGCCACTCTGTGCT 1124  
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US-10-450-097-30  
; Sequence 30, Application US/10450097  
; Publication No. US20040110252A1  
; GENERAL INFORMATION:  
; APPLICANT: Septegen Ltd  
; TITLE OF INVENTION: Yeast-Based Assay  
; FILE REFERENCE: DE/p701948PCT  
; CURRENT APPLICATION NUMBER: US/10/450,097  
; PRIOR FILING DATE: 2003-05-29  
; PRIOR FILING DATE: 2000-12-08  
; NUMBER OF SEQ ID NOS: 53  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 30  
; LENGTH: 10042  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:PREPXi-CRHR  
US-10-450-097-30

Query Match 73.0%; Score 1154.2; DB 7; Length 10042;  
Best Local Similarity 93.3%; Pred. No. 5.4e-310;  
Matches 1253; Conservative 0; Mismatches 3; Indels 87; Gaps 1;  
Qy 75 CCGAGAGTGGAGGGACCGCGAGCTCCGTCTGCTCAAGGCCCTTCTCTTGGGGCT 134  
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Qy 135 GAACCCCGTCTGCTCCCTCCAGGACGAGCACTGGAGAGCTGCTCCCTGGCCAGCAA 194  
Db 1287 GAACCCCGTCTGCTCCCTCCAGGACGAGCACTGGAGAGCTGCTCCCTGGCCAGCAA 1346

Qy 195 CATCTCAGGACTGCACTGCAACGCGATCCGTGGACCTCATTTGGCACCTGCTGGGCCCGCGAG 254  
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Qy 795 GGGCTCTACCTGCACACAGCCATCGTGTCTCACTTCCACTGACCGGCTGGCGCAAAATG 854  
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Qy 855 GATGTTTCATCTGCAATTTGGCTGGGCTGTGCGCTTCCCATCATTTGGGCTGTGGGCCAATGG 914  
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Qy 382 GAGTGCAGAGATCTCAATGAGAGAGAAAAAGCAAGGTGCATCAATGTCGAGTC 441  
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Db 433 -----AGGAGCATCCGGTGCCTGCGGA 453  
Qy 622 AACATCATCACTGGACCTCATCTCGCCTTTCATCTGGCGCAACGCCACCTGGTTCGTG 681  
Db 454 AACATCATCACTGGACCTCATCTCGCCTTTCATCTGGCGCAACGCCACCTGGTTCGTG 513  
Qy 682 GTCCAGCTAACCATGAGCCCCGAGGCTCCACAGAGCAACGTGGGCTGGTGCAGGTTGGTG 741  
Db 514 GTCCAGCTAACCATGAGCCCCGAGGCTCCACAGAGCAACGTGGGCTGGTGCAGGTTGGTG 573  
Qy 742 ACAGCGGCTTACAACTATTCATGATGACCAACTTCTTCTGGATGTTGGCGAGGCGTGC 801  
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Qy 862 ATCTGATTTGGCTGGGCTGGCCCTTCCCATCAATTTGGCCCTGGGCCATTGGGAAAGCTG 921  
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US-09-853-386-107  
; Sequence 107, Application US/09853386  
; Patent No. US20020049151A1  
; GENERAL INFORMATION:  
; APPLICANT: Murphy, Evelyn  
; APPLICANT: Bresnihan, Barry  
; APPLICANT: Conneely, Orla  
; APPLICANT: Fitzgerald, Oliver  
; TITLE OF INVENTION: Therapeutic Approaches to Diseases by Suppression of the NURR  
; TITLE OF INVENTION: Subfamily of Nuclear Transcription Factors  
; FILE REFERENCE: P01972051  
; CURRENT APPLICATION NUMBER: US/09/853,386  
; PRIOR FILING DATE: 2001-05-11  
; PRIOR APPLICATION NUMBER: US 60/203645  
; PRIOR FILING DATE: 2000-05-12  
; NUMBER OF SEQ ID NOS: 153  
; SOFTWARE: Patent in version 3.1  
; SEQ ID NO 107  
; LENGTH: 1206  
; TYPE: DNA  
; ORGANISM: HUMAN  
US-09-853-386-107

Query Match 66.8%; Score 1057; DB 3; Length 1206;  
Best Local Similarity 90.3%; Pred. No. 3.2e-283;  
Matches 1206; Conservative 0; Mismatches 0; Indels 129; Gaps 2;

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GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

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Perfect score: 1582  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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9	1396.4	88.3	2536	3	US-09-799-978-1
10	1335	84.4	1335	3	US-09-016-434-1360
11	1283	81.1	1380	2	US-08-110-286A-1
12	1188	75.1	1285	3	US-09-799-978-3
13	1149.4	72.7	1248	3	US-09-826-509-482
14	1057	66.8	1206	3	US-09-799-978-7
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16	1035.2	65.4	1411	3	US-09-580-734-5
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24	919	58.1	1146	3	US-09-799-978-5

25	810.2	51.2	1422	3	US-09-799-978-41	Sequence 41, Appl
26	662.6	41.9	1338	3	US-09-799-978-33	Sequence 33, Appl
27	622	39.3	1442	3	US-09-799-978-35	Sequence 35, Appl
28	617.8	39.1	1248	3	US-09-799-978-29	Sequence 29, Appl
29	559.6	35.4	1600	3	US-09-799-978-11	Sequence 11, Appl
30	557.8	35.3	1468	2	US-08-381-433A-7	Sequence 7, Appl
31	557.8	35.3	1468	3	US-09-881-401-7	Sequence 7, Appl
32	557.8	35.3	2110	3	US-09-016-434-1070	Sequence 1070, Ap
33	557.8	35.3	2110	3	US-09-799-978-9	Sequence 9, Appl
34	557	35.2	1558	3	US-09-799-978-13	Sequence 13, Appl
35	545	34.5	1626	2	US-08-381-433A-3	Sequence 3, Appl
36	545	34.5	1626	3	US-09-799-978-17	Sequence 17, Appl
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40	541.2	34.2	2617	3	US-09-799-978-25	Sequence 25, Appl
41	541	34.2	1514	3	US-09-799-978-19	Sequence 19, Appl
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44	531	33.6	1374	3	US-08-374-009-9	Sequence 9, Appl
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ALIGNMENTS

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; Patent No. 639315  
; GENERAL INFORMATION:  
; APPLICANT: Perrin, Marilyn H.  
; APPLICANT: Chen, Ruoping  
; APPLICANT: Lewis, Kathy A.  
; APPLICANT: Vale Jr., Wylie W.  
; APPLICANT: Donaldson, Cynthia J.  
; APPLICANT: Sawchenko, Paul  
; TITLE OF INVENTION: Cloning and Recombinant Production of  
; FILE REFERENCE: P41-90002  
; CURRENT APPLICATION NUMBER: US/08/482,746B  
; EARLIER FILING DATE: 1995-06-07  
; EARLIER APPLICATION NUMBER: US 08/374,009  
; EARLIER FILING DATE: 1995-01-17  
; EARLIER APPLICATION NUMBER: US 08/353,537  
; EARLIER FILING DATE: 1994-12-09  
; EARLIER APPLICATION NUMBER: PCT/US94/05908  
; EARLIER FILING DATE: 1994-05-25  
; EARLIER APPLICATION NUMBER: US 08/110,286  
; EARLIER FILING DATE: 1993-08-23  
; EARLIER APPLICATION NUMBER: US 08/079,320  
; EARLIER FILING DATE: 1993-06-18  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 14  
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; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (82)...(1413)  
; OTHER INFORMATION: CRF-R splice-variant insert fragment inserted  
; OTHER INFORMATION: between nucleotides 516-517 of SEQ ID NO:1.  
; OTHER INFORMATION: /note= "this sequence is contained in clone  
; OTHER INFORMATION: "CRF-R2".  
US-08-482-746-14

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Qy 661 CGCAACGCCACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720  
Db 661 CGCAACGCCACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720  
Qy 721 GTGGGCTGTGAGGTTGTGAGCAGCGCCTCAACATCTCAATGAGCAACATCTTCTTC 780  
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Qy 781 TGGATGTTCCGCGAGGCTGCTACCTGCACACAGCCATCGTGTCACTACTCCACTGAC 840  
Db 781 TGGATGTTCCGCGAGGCTGCTACCTGCACACAGCCATCGTGTCACTACTCCACTGAC 840  
Qy 841 CCGCTGCGCAATGGAATGTTCACTGCAATGCTGGGCTGCTGCTGCTGCTGCTGCTGCTG 900  
Db 841 CCGCTGCGCAATGGAATGTTCACTGCAATGCTGGGCTGCTGCTGCTGCTGCTGCTGCTG 900  
Qy 901 GCCTGGGCCAATGGGAAGCTGTAAGCAATGAGAGTGTGTTGGTGGCAAAAGGCTT 960  
Db 901 GCCTGGGCCAATGGGAAGCTGTAAGCAATGAGAGTGTGTTGGTGGCAAAAGGCTT 960  
Qy 961 GGGGTGTACACGACTACATCTACCGGGGCGCCATGATCTGCTGCTGCTGCTGCTGCTG 1020  
Db 961 GGGGTGTACACGACTACATCTACCGGGGCGCCATGATCTGCTGCTGCTGCTGCTGCTG 1020  
Qy 1021 ATCTTCCTTTTCAACATCGTCCGATCCTCATGACCAAGCTCCGGGCACTCCACAGCTT 1080  
Db 1021 ATCTTCCTTTTCAACATCGTCCGATCCTCATGACCAAGCTCCGGGCACTCCACAGCTT 1080  
Qy 1081 GAGACCAATTCAGTACAGGAAGGCTGTGAAGGCACTCTGCTGCTGCTGCTGCTGCTG 1140  
Db 1081 GAGACCAATTCAGTACAGGAAGGCTGTGAAGGCACTCTGCTGCTGCTGCTGCTGCTG 1140

Qy 1141 ATCACCTACATGCTGTTCTTCTGTCATCCCGGGAGGATGAGTCTCCCGGTCGTCCTTC 1200  
Db 1141 ATCACCTACATGCTGTTCTTCTGTCATCCCGGGAGGATGAGTCTCCCGGTCGTCCTTC 1200  
Qy 1201 ATCTACTTCAACTCCTTCTGGAATCTCTTCCAGGGCTTCTTGTGTGTGTGTGTGTGT 1260  
Db 1201 ATCTACTTCAACTCCTTCTGGAATCTCTTCCAGGGCTTCTTGTGTGTGTGTGTGTGT 1260  
Qy 1261 TTCTCTCAATAGTGAAGTCCGTTCTGCCATCCGGAAGAGTGGCACTGGTGGCAGGCAAG 1320  
Db 1261 TTCTCTCAATAGTGAAGTCCGTTCTGCCATCCGGAAGAGTGGCACTGGTGGCAGGCAAG 1320  
Qy 1321 CACTCGATCCGTCGCGAGTCCGTCGTCATGCCATCCCTCCCAACCCCGTGTTC 1380  
Db 1321 CACTCGATCCGTCGCGAGTCCGTCGTCATGCCATCCCTCCCAACCCCGTGTTC 1380  
Qy 1381 AGCTTTACAGCATCAAGCAGTCCACAGCAGTCTGAGCTGGCAGGTCTATGGAGAGCCCC 1440  
Db 1381 AGCTTTACAGCATCAAGCAGTCCACAGCAGTCTGAGCTGGCAGGTCTATGGAGAGCCCC 1440  
Qy 1441 CAAAGAGCTGTGGCTGGGGGATGAGCGCCAGGCTCCCTGACCACTGCTGCTGAGGT 1500  
Db 1441 CAAAGAGCTGTGGCTGGGGGATGAGCGCCAGGCTCCCTGACCACTGCTGCTGAGGT 1500  
Qy 1501 GACCTGTAGGTCTCATGCCCCTCTCCCGCAGGAGAGTGGCAGCTGACAGCCCTGGGGGG 1560  
Db 1501 GACCTGTAGGTCTCATGCCCCTCTCCCGCAGGAGAGTGGCAGCTGACAGCCCTGGGGGG 1560  
Qy 1561 CCGCTCTCCCTGACGCGGTG 1582  
Db 1561 CCGCTCTCCCTGACGCGGTG 1582

## RESULT 2

US-09-580-734-14  
; Sequence 14, Application US/09580734  
; Patent No. 6482608  
; GENERAL INFORMATION:  
; APPLICANT: Perrin, Marilyn H.  
; APPLICANT: Chen, Ruoping  
; APPLICANT: Lewis, Kathy A.  
; APPLICANT: Vale Jr., Wylie W.  
; APPLICANT: Donaldson, Cynthia J.  
; APPLICANT: Sawchenko, Paul  
; TITLE OF INVENTION: Cloning and Recombinant Production of  
; FILE REFERENCE: Salk1748  
; CURRENT APPLICATION NUMBER: US/09/580,734  
; CURRENT FILING DATE: 2000-05-26  
; PRIOR FILING DATE: 1998-11-12  
; PRIOR APPLICATION NUMBER: US 08/374,009  
; PRIOR FILING DATE: 1995-01-17  
; PRIOR APPLICATION NUMBER: US 08/353,537  
; PRIOR FILING DATE: 1994-12-09  
; PRIOR APPLICATION NUMBER: PCT/US94/05908  
; PRIOR FILING DATE: 1993-05-25  
; PRIOR APPLICATION NUMBER: US 08/110,286  
; PRIOR FILING DATE: 1993-08-23  
; PRIOR APPLICATION NUMBER: US 08/079,320  
; PRIOR FILING DATE: 1993-06-18  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 14  
; LENGTH: 1582  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (82)...(1413)  
; OTHER INFORMATION: CRP-R splice-variant insert fragment inserted  
; OTHER INFORMATION: between nucleotides 516-517 of SEQ ID NO:1.



; OTHER INFORMATION: /note= "This sequence is contained in clone  
; OTHER INFORMATION: "CRF-R2"."  
US-09-580-734-14

Query Match 100.0%; Score 1582; DB 3; Length 1582;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1582; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 CGAGCCGCGAGCCGCGCGGTTCTCTGGGATGTCGAGACCCGGGCAATTCAGGAC 60  
DB 1 CGAGCCGCGAGCCGCGCGGTTCTCTGGGATGTCGAGACCCGGGCAATTCAGGAC 60  
  
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DB 61 GGTAGCCGAGCGAGCCGCGGATGGGAGGCGACCCCGAGCTCCGTCTCGTAGGGCCCTT 120  
  
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DB 121 CTCCTTCTGGGGCTGAACCCCGCTCTCTGCTCCCTCCAGAGCCAGACATGCGAGAGCCTG 180  
  
QY 181 TCCCTGGCCAGCAACATCTCAGGACTGCGAGTGCAGCGCATCCGTGGACCTCATTTGGCACC 240  
DB 181 TCCCTGGCCAGCAACATCTCAGGACTGCGAGTGCAGCGCATCCGTGGACCTCATTTGGCACC 240  
  
QY 241 TGTGCGCCCGCAGCCCTGCGGGGCGAGTGTAGTGGTTCGGCCCTGCGCTTTTCTAT 300  
DB 241 TGTGCGCCCGCAGCCCTGCGGGGCGAGTGTAGTGGTTCGGCCCTGCGCTTTTCTAT 300  
  
QY 301 GGTGTCGGCTTACAAATACCAACAAATGGCTACCGGAGTGCTGCGCAATGCGAGCTGG 360  
DB 301 GGTGTCGGCTTACAAATACCAACAAATGGCTACCGGAGTGCTGCGCAATGCGAGCTGG 360  
  
QY 361 GCGCCCGCGGTGAATTAATCTCCGAGTGCAGGAGATCTCAATGAGGAGAAAAAGCAAG 420  
DB 361 GCGCCCGCGGTGAATTAATCTCCGAGTGCAGGAGATCTCAATGAGGAGAAAAAGCAAG 420  
  
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DB 421 GTGCACTACATGTGCGAGTCAATCAACTACTGCGGCCACTGTATCTCCCTGGTGGCC 480  
  
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DB 481 CTCCTGGTGGCTTTGTCTCTTCTGCGCTCAGGCCAGGCTGACCCATTGSGGTGAC 540  
  
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DB 601 AGGAGCATCCGGTGCCTGCGAAACATCATCACTGGAACCTCATCTCCGCTTCATCCTG 660  
  
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DB 661 CGCAACGCCACCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 720  
  
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DB 721 GTGGGCTGGTGGAGTGGTGACAGCGCCCTCAAACTACTTCAATGAGCAAACTTCTTC 780  
  
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DB 781 TGGATGTTGCGGAGGGCTCTACCTGCAACAGCCATCGTGTCTCACTACTCACTGAC 840  
  
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DB 901 GCCTGGGCCATTGGGAAGCTGTACTAGCAAAATGAGAAGTGGTGTGGCAAAAGCCCT 960  
  
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DB 961 GGGGTGTACCCGACTACATCTACAGGGCCCATGATCTGTCTCTGTGATCAATTTTC 1020  
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DB 1021 ATCTTCTCTTTTCAACATCGTCCGCATCTCTCATGACCAAGCTCCGGGCATCCACAGCTCT 1080  
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DB 1081 GAGACCATTCAGTACAGGAAGGCTGTGAAGCCACTCTGGTGTCTGCTGCTCTGGGC 1140  
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DB 1141 ATCACTTACATGCTGTTCTTCTGTCATCCCGGGAGGATGAGGTCTCCCGGGTCTCTTC 1200  
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DB 1561 CCGCTCTCCCGCTGACGCGGTG 1582

RESULT 3  
US-08-374-009-14  
; Sequence 14, Application US/08374009A  
; Patent No. 6495343  
; GENERAL INFORMATION:  
; APPLICANT: Perrin, Marilyn H.  
; APPLICANT: Chen, Ruoping  
; APPLICANT: Lewis, Kathy A.  
; APPLICANT: Vale Jr., Wylie W.  
; APPLICANT: Donaldson, Cynthia J.  
; APPLICANT: Sawchenko, Paul  
; TITLE OF INVENTION: Cloning and Recombinant Production of  
; FILE REFERENCE: P41 9886  
; CURRENT APPLICATION NUMBER: US/08/374,009A  
; CURRENT FILING DATE: 1995-01-17  
; EARLIER APPLICATION NUMBER: US 08/353,537  
; EARLIER FILING DATE: 1994-12-09  
; EARLIER APPLICATION NUMBER: US 08/079,320  
; EARLIER FILING DATE: 1993-06-18  
; EARLIER APPLICATION NUMBER: US 08/110,286  
; EARLIER FILING DATE: 1993-08-23  
; EARLIER APPLICATION NUMBER: PCT/US94/05908  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 14  
; LENGTH: 1582  
; TYPE: DNA

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/ ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (82)...(1413)
; OTHER INFORMATION: CRP-R splice-variant insert fragment inserted
; OTHER INFORMATION: between nucleotides 516-517 of SEQ ID NO:1.
; OTHER INFORMATION: /note= "This sequence is contained in clone
; OTHER INFORMATION: "CRP-R2".
US-08-374-009-14

Query Match      100.0%; Score 1582; DB 3; Length 1582;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1582; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGAGCCGCGAGCCGCGCGGTTCTCTGGGATGTCCGTAGGACCGGGCATTCAGGAC 60
Db 1 CGAGCCGCGAGCCGCGCGGTTCTCTGGGATGTCCGTAGGACCGGGCATTCAGGAC 60

QY 61 GGTAGCCGAGCGAGCCGAGGATGGGAGGACCCCGCAGCTCCGTCTCGTCAAGGCCCTT 120
Db 61 GGTAGCCGAGCGAGCCGAGGATGGGAGGACCCCGCAGCTCCGTCTCGTCAAGGCCCTT 120

QY 121 CTCTCTCTGGGGCTGAACCCCGCTCTCTGCTCCCTCAGGACCGAGCACTGCGAGGCTG 180
Db 121 CTCTCTCTGGGGCTGAACCCCGCTCTCTGCTCCCTCAGGACCGAGCACTGCGAGGCTG 180

QY 181 TCCTGGCGAGCAACATCTCAGGACTGCAAGTGCATCGCATCCGTGCGTCAAGGCCCTT 240
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QY 241 TGTGCGCCCGCAGCCCTGCGGGGAGCTAGTGGTTGCGGCCCTGCGCTCTTTTCTAT 300
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QY 361 GCGCCCGCGGTGAATTTACTCCGAGTGCAGGAGATCTCAATGAGGAGAAAAAGCAAG 420
Db 361 GCGCCCGCGGTGAATTTACTCCGAGTGCAGGAGATCTCAATGAGGAGAAAAAGCAAG 420

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QY 481 CTCTGTGGCTTTGTCTCTTTCTGCGCTCAGGCCAGGCTGCAACCCATGGGGTGAC 540
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QY 541 CAGGCAGATGGAGCCCTGGAGGTGGGGCTCCATGGAGTGGTCCCATTTTCAGGTTGGA 600
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QY 601 AGGAGCATCCGCTGCGTCCGAAACATCATCTCACTGGAACCTCATCTCGGCTTCATCCTG 660
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QY 721 GTGGCTGTGTGAGGTGTGACAGCGGCTCAACTACTTCTCATGTGACCAACTTCTTC 780
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QY 841 CGGCTCGCAAAATGGATGTTTCACTGCAATTTGGCTGGGGTGTGCGCTTCCCATCATTTG 900
Db 841 CGGCTCGCAAAATGGATGTTTCACTGCAATTTGGCTGGGGTGTGCGCTTCCCATCATTTG 900
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## RESULT 4

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US-09-191-724-14
; Sequence 14, Application US/09191724
; Patent No. 6638905
; GENERAL INFORMATION:
; APPLICANT: Perrin, Marilyn H.
; APPLICANT: Chen, Ruoping
; APPLICANT: Lewis, Kathy A.
; APPLICANT: Vale Jr., Wylie W.
; APPLICANT: Donaldson, Cynthia J.
; APPLICANT: Sawchenko, Paul
; TITLE OF INVENTION: Cloning and Recombinant Production of
; FILE REFERENCE: Salk1748
; CURRENT APPLICATION NUMBER: US/09/191,724
; CURRENT FILING DATE: 1998-11-12
; EARLIER APPLICATION NUMBER: US 08/374,009
; EARLIER FILING DATE: 1995-01-17
; EARLIER APPLICATION NUMBER: US 08/353,537
; EARLIER FILING DATE: 1994-12-09
; EARLIER APPLICATION NUMBER: PCT/US94/05908
; EARLIER FILING DATE: 1993-05-25
; EARLIER APPLICATION NUMBER: US 08/110,286
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RESULT 7
US-08-374-009-1
; Sequence 1, Application US/08374009A
; Patent No. 6495343
; GENERAL INFORMATION:
; APPLICANT: Perrin, Marilyn H.
; APPLICANT: Chen, Ruoping
; APPLICANT: Lewis, Kathy A.
; APPLICANT: Vale Jr., Wylie W.
; APPLICANT: Donaldson, Cynthia J.
; APPLICANT: Sawchenko, Paul
; TITLE OF INVENTION: Cloning and Recombinant Production of
; TITLE OF INVENTION: CRF Receptor(s)
; FILE REFERENCE: P41 9886
; CURRENT APPLICATION NUMBER: US/08/374,009A
; CURRENT FILING DATE: 1995-01-17
; EARLIER APPLICATION NUMBER: US 08/353,537
; EARLIER FILING DATE: 1994-12-09
; EARLIER APPLICATION NUMBER: US 08/079,320
; EARLIER FILING DATE: 1993-06-18
; EARLIER APPLICATION NUMBER: US 08/110,286
; EARLIER FILING DATE: 1993-08-23
; EARLIER APPLICATION NUMBER: PCT/US94/05908
; EARLIER FILING DATE: 1994-05-25
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 1495
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (82)...(1326)
; OTHER INFORMATION: /product = "Human pituitary CRF-receptor"
; OTHER INFORMATION: /note= "This sequence is encoded by clone
; OTHER INFORMATION: "CRF-R1".
US-08-374-009-1

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Best Local Similarity 94.5%; Pred. No. 0;
Matches 1495; Conservative 0; Mismatches 0; Indels 87; Gaps 1;

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DB      61  GGTAGCGGAGCGAGCGCGGATGGAGGCGCACCCGCGAGCTCCGTCCTCGTCAAGGCCCTT 120

QY      121  CTCCTTCTGGGGCTGAACCCCGTCTCTGCTCCCTCCAGACCGAGCACTGGAGGCGCTG 180
DB      121  CTCCTTCTGGGGCTGAACCCCGTCTCTGCTCCCTCCAGACCGAGCACTGGAGGCGCTG 180

QY      181  TCCTCGCCAGCAACATCTCAGAGCTGCAAGCGCATCCGTCGAGACCTCATTTGGCACC 240
DB      181  TCCTCGCCAGCAACATCTCAGAGCTGCAAGCGCATCCGTCGAGACCTCATTTGGCACC 240

QY      241  TGTGCGCCCGCGAGCCCTGCGGGGCGAGTAGTGGTTGCGGCCCTGCCCTTTTCTAT 300
DB      241  TGTGCGCCCGCGAGCCCTGCGGGGCGAGTAGTGGTTGCGGCCCTGCCCTTTTCTAT 300

QY      301  GGTGTGGCTACAAATACCAAAATGGCTACGGGAGTGCTTGGCAATGGCAGCTGG 360
DB      301  GGTGTGGCTACAAATACCAAAATGGCTACGGGAGTGCTTGGGCAATGGCAGCTGG 360

QY      361  GCGCGCCGCGTGAATTACTCCGAGTGCAGAGATCTCAATGAGGAGAAAAAGCAAG 420
DB      361  GCGCGCCGCGTGAATTACTCCGAGTGCAGAGATCTCAATGAGGAGAAAAAGCAAG 420

QY      421  GTGCATACCATGTGCGAGTCATCACTACCTGGGCGACTGTATCTCCCTGGTGGCC 480
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DB      421  GTGCATACCATGTGCGAGTCATCACTACCTGGGCGACTGTATCTCCCTGGTGGCC 480
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DB      514  ----- 513
QY      601  AGGAGCATCCGGTGCCTGCGAAACATCATCTGGAACCTCATCTCCGCTTCATCTCTG 660
DB      514  AGGAGCATCCGGTGCCTGCGAAACATCATCTGGAACCTCATCTCCGCTTCATCTCTG 573
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DB      634  GTGGGCTGGTGCAGGTTCGTGACAGCCGCTCAACACTACTTCCATGTGACCAACTTCTTC 693
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DB      694  TGGATGTTCCGGAGAGGCTGTACTGCAACAGCCATCGTGTCTACCTACTCCACTGAC 753
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DB      754  CGGCTGCGCAAAATGGATGTTTCATCTGCAATTTGGTGGGTGTGCCCTTCCCATCATTTG 813
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DB      814  GCCTGGGCCAATTTGGGAAGCTGTACTACGACAATGAGAAGTGTGTGGTTTGGCAAAAGCCCT 873
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QY      1321  CACTCAATCCGTGCCGAGTGGCCCGTGCATGTTCATCCCACTCCCAACCCCGTGTCT 1380
DB      1234  CACTCAATCCGTGCCGAGTGGCCCGTGCATGTTCATCCCACTCCCAACCCCGTGTCT 1293
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DB      1294  AGCTTTTCAAGCATCAAGCAGTCCACAGCAGTCTGAGCTGGCAGGTGATGGAGAGCCCC 1353
QY      1441  CAAAGAGCTGTGCTGGGGGATGAGCGGCAGGCTCCCTGACCACTGCTGCTGTGGAGGT 1500
DB      1354  CAAAGAGCTGTGCTGGGGGATGAGCGGCAGGCTCCCTGACCACTGCTGCTGTGGAGGT 1413
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DB      1414  GACCTGTAGGTCTCATGCCCCACTCCCCCAAGAGAGTGGGCACTGACAGCTGGGGGGG 1473
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QY 1441 CAAAGAGCTGTGCTGGGGGATGACGGCCAGGCTCCCTGACCAACCTGCTCTGTGGAGGT 1500  
Db CAAAGAGCTGTGCTGGGGGATGACGGCCAGGCTCCCTGACCAACCTGCTCTGTGGAGGT 1413  
QY 1501 GACCTGTAGGTCTCATGCCCACTCCCCAGGAGAGCTGGCACTGACAGCCCTGGGGGGG 1560  
Db GACCTGTAGGTCTCATGCCCACTCCCCAGGAGAGCTGGCACTGACAGCCCTGGGGGGG 1473  
QY 1561 CCGCTCTCCCCCTGCAGCCGTG 1582  
Db CCGCTCTCCCCCTGCAGCCGTG 1495  
RESULT 9  
US-09-799-978-1  
; Sequence 1, Application US/09799978  
; Patent No. 6670140  
; GENERAL INFORMATION:  
; APPLICANT: The Procter & Gamble Company  
; APPLICANT: Isefort, Robert  
; APPLICANT: Sheldon, Russell  
; TITLE OF INVENTION: Methods for Identifying Compounds for Regulating Muscle Mass or  
; TITLE OF INVENTION: Function Using Corticotropin Releasing Factor Receptors  
; FILE REFERENCE: 8448  
; CURRENT APPLICATION NUMBER: US/09/799,978  
; CURRENT FILING DATE: 2001-03-06  
; NUMBER OF SEQ ID NOS: 44  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 1  
; LENGTH: 2536  
; TYPE: DNA  
; ORGANISM: homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (227)..(1474)  
US-09-799-978-1  
Query Match 88.3%; Score 1396.4; DB 3; Length 2536;  
Best Local Similarity 94.4%; Pred. No. 0;  
Matches 1494; Conservative 0; Mismatches 1; Indels 87; Gaps 1;  
QY 1 CGAGCCGCGAGCGCCGCGGTCTCTGGGATGTCCTGAGACCCGGGCAATTCAGGAC 60  
Db CGAGCCGCGAGCGCCGCGGTCTCTGGGATGTCCTGAGACCCGGGCAATTCAGGAC 205  
QY 61 GGTAGCGGAGCGAGCGCGAGGATGGGAGGCGACCCGAGTCCGTCTGTCAGGCGCCTT 120  
Db GGTAGCGGAGCGAGCGCGAGGATGGGAGGCGACCCGAGTCCGTCTGTCAGGCGCCTT 265  
QY 121 CTCTTTCTGGGGCTGAACCCCGTCTCTGCTCTCCAGGACCGACACTGCGAGAGCCTG 180  
Db CTCTTTCTGGGGCTGAACCCCGTCTCTGCTCTCCAGGACCGACACTGCGAGAGCCTG 325  
QY 181 TCCCTGGCAGCAACATCTCAGGACTGCAAGTCAACGCACTCGTGGACCTCAATGGCACC 240  
Db TCCCTGGCAGCAACATCTCAGGACTGCAAGTCAACGCACTCGTGGACCTCAATGGCACC 385  
QY 241 TGTGCCCCCGAGCCCTGGGGGAGCTAGTGGTTGGGCCCTGCGCCCTGCTTTTCTAT 300  
Db TGTGCCCCCGAGCCCTGGGGGAGCTAGTGGTTGGGCCCTGCGCCCTGCTTTTCTAT 445  
QY 301 GGTGTCGGCTACAAATACCAAAATGGTACCGGGAGTGGCTGGCCAAATGGCAGCTG 360  
Db GGTGTCGGCTACAAATACCAAAATGGTACCGGGAGTGGCTGGCCAAATGGCAGCTG 505  
QY 361 GCGCCCGCGGTGAATTAATCCAGAGTCCAGGAGATCTCAATGAGGAGAAAAAACAAG 420  
Db GCGCCCGCGGTGAATTAATCCAGAGTCCAGGAGATCTCAATGAGGAGAAAAAACAAG 565  
QY 421 GTGCACTACATGTCCGAGTCAATCAACTACCTGGGCGCACTGTATCTCCCTGTGGCC 480  
Db GTGCACTACATGTCCGAGTCAATCAACTACCTGGGCGCACTGTATCTCCCTGTGGCC 625

QY 481 CTCTGCTGGCTTTGTCTCTCTTTCTGCGGCTCAGGCCAGGCTGCACCCATTGGGGTGAC 540  
Db CTCTGCTGGCTTTGTCTCTCTTTCTGCGGCTC----- 658  
QY 541 CAGGCAGATGAGACCCCTGAGAGGTGGGGGTCCATGAGGTGGTGGCCCAATTCAGGTTGCA 600  
Db ----- 658  
QY 601 AGGAGCATCCGGTGCCTGCGAAACATCATCTGGAACCTCATCTCCGCTTCATCCCTG 660  
Db AGGAGCATCCGGTGCCTGCGAAACATCATCTGGAACCTCATCTCCGCTTCATCCCTG 718  
QY 661 CGCAACGCCACCTGGTTCTGTGGTCCAGCTAAACATGAGCCCCGAGGTCCACAGAGCAAC 720  
Db CGCAACGCCACCTGGTTCTGTGGTCCAGCTAAACATGAGCCCCGAGGTCCACAGAGCAAC 778  
QY 721 GTGGGCTGTGACAGGTGTGTGACAGCGGCTCAACTACTTTCATGTGACCAACTTCTTC 780  
Db GTGGGCTGTGACAGGTGTGTGACAGCGGCTCAACTACTTTCATGTGACCAACTTCTTC 838  
QY 781 TGGATGTTCCGGGAGGGCTGCTACCTGACACAGCCATCGTCTCACTTCTCCACTGAC 840  
Db TGGATGTTCCGGGAGGGCTGCTACCTGACACAGCCATCGTCTCACTTCTCCACTGAC 898  
QY 841 CCGCTCGCAAAATGGATGTTCTATCTGCAATTGGCTGGGGTGTGCCCTTCCCCATCATTTGTG 900  
Db CCGCTCGCAAAATGGATGTTCTATCTGCAATTGGCTGGGGTGTGCCCTTCCCCATCATTTGTG 958  
QY 901 GCTTGGGCCAATTTGGGAAGCTGTACTACGAAATGAGAAAGTGTGTGGTGGCAAAAGCCCT 960  
Db GCTTGGGCCAATTTGGGAAGCTGTACTACGAAATGAGAAAGTGTGTGGTGGCAAAAGCCCT 1018  
QY 961 GGGGTGTACACCGACTACATCTACGAGGGCCCAATGATCTCTGCTCTGATCAATTTTC 1020  
Db GGGGTGTACACCGACTACATCTACGAGGGCCCAATGATCTCTGCTCTGATCAATTTTC 1078  
QY 1021 ATCTTCTCTTTTCAACATCTCGCGCATCTCATGACCAAGCTCCGGGCATCCACCACTGT 1080  
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QY 1081 GAGACCAATTCAGTACAGGAAGCTGTGAAAGCACTCTGCTGTCTGCTGCTCTCTGGGC 1140  
Db GAGACCAATTCAGTACAGGAAGCTGTGAAAGCACTCTGCTGTCTGCTGCTCTCTGGGC 1198  
QY 1141 ATCACTCACTGCTGTCTTCTGCTCAATCCCGGGGAGGATGAGGTCTCCCGGCTGCTTC 1200  
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QY 1201 ATCTACTTCAACTCTCTTCTGGAATCTTTCAGGGCTTCTTTGTGTCTGTGTCTACTGT 1260  
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QY 1261 TTCCTCAATGAGAGTCCGTTCTGCAATCCGGAAGAGGTGGCAACGGTGGGAGGCAAG 1320  
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QY 1321 CACTCGATCCGTCGCGAGTGGCCGTGCAATGTCATCCCACTCCCAACCCGCTGTC 1380  
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QY 1381 AGCTTTTCAACGATCAAGCAGTCCACAGCAGTCTGAGCTGGGAGGTCATGAGAGAGCCCC 1440  
Db AGCTTTTCAACGATCAAGCAGTCCACAGCAGTCTGAGCTGGGAGGTCATGAGAGAGCCCC 1498  
QY 1441 CAAAGAGCTGTGGCTGGGGGATGACGGCCAGGCTCCCTGACCAACCTGCTGTGGAGGT 1500  
Db CAAAGAGCTGTGGCTGGGGGATGACGGCCAGGCTCCCTGACCAACCTGCTGTGGAGGT 1558  
QY 1501 GACCTGTAGGTCTCATGCCCACTCCCCAGGAGAGCTGGCACTGACAGCCCTGGGGGGG 1560  
Db GACCTGTAGGTCTCATGCCCACTCCCCAGGAGAGCTGGCACTGACAGCCCTGGGGGGG 1618  
QY 1561 CCGCTCTCCCCCTGCAGCCGTG 1582

Db 1619 CCGCTCTCCCTCGACCGGTG 1640  
RESULT 10  
US-09-016-434-1360  
; Sequence 1360, Application US/09016434  
; Patent No. 6500938  
; GENERAL INFORMATION:  
; APPLICANT: Janice Au-Young  
; APPLICANT: Jeffrey J. Sellhammer  
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING  
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION  
; NUMBER OF SEQUENCES: 1490  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
; STREET: 3174 PORTER DRIVE  
; CITY: PALO ALTO  
; STATE: CALIFORNIA  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/016,434  
; FILING DATE: HEREWITH  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Zeller, Karen J.  
; REGISTRATION NUMBER: 37,071  
; REFERENCE/DOCKET NUMBER: PA-0002 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (650) 855-0555  
; TELEFAX: (650) 845-4166  
; INFORMATION FOR SEQ ID NO: 1360:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1335 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; IMMEDIATE SOURCE:  
; LIBRARY: GENBANK  
; CLONE: 9408691  
US-09-016-434-1360  
Query Match 84.4%; Score 1335; DB 3; Length 1335;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 82 ATGGGAGGGGACCCGAGCTCCGCTCGTCAAGGCCCTTCTCTCTTCTGGGGCTGAACCCC 141  
Db 1 ATGGGAGGGGACCCGAGCTCCGCTCGTCAAGGCCCTTCTCTCTTCTGGGGCTGAACCCC 60  
QY 142 GTCTCTGCTCCCTCAGAGACAGACTGCGAGAGCCCTGCTCCCTGGGCAGCAATCTCA 201  
Db 61 GTCTCTGCTCCCTCAGAGACAGACTGCGAGAGCCCTGCTCCCTGGGCAGCAATCTCA 120  
QY 202 GGAGTGCAGTGAACGATCCGCTGACCTCATTTGGACCTGCTGGCCCGCCGCTGGG 261  
Db 121 GGAGTGCAGTGAACGATCCGCTGACCTCATTTGGACCTGCTGGCCCGCCGCTGGG 180  
QY 262 GGGCAGCTAGTGTGTGGCCCTGCTCCCTGCTCTTCTATGCTGTCCGCTACAAATACACA 321  
Db 181 GGGCAGCTAGTGTGTGGCCCTGCTCCCTGCTCTTCTATGCTGTCCGCTACAAATACACA 240  
QY 322 AACAAATGGCTACCGGGAGTGCCTTGGCCAAATGGCAGCTGGGCCCGCCGCTGAATTAATCC 381

Db 241 AACAAATGGCTACCGGGAGTGCCTTGGCCAAATGGCAGCTGGGCCCGCCGCTGAATTAATCC 300  
QY 382 GAGTGCAGGAGATCCTCAATGAGGAGAAAAAAGCAAGGTGCATCAACATGTCGAGTC 441  
Db 301 GAGTGCAGGAGATCCTCAATGAGGAGAAAAAAGCAAGGTGCATCAACATGTCGAGTC 360  
QY 442 ATCATCAACTACCTGGGCCACTGTATCTCCCTGGTGGCCCTCTCTGGTGGCTTTGCTTC 501  
Db 361 ATCATCAACTACCTGGGCCACTGTATCTCCCTGGTGGCCCTCTCTGGTGGCTTTGCTTC 420  
QY 502 TTTCTCGGCTCAGGCCAGGCTGCACCCATTGGGGTGACCCAGCAGATGAGGCCCTGGAG 561  
Db 421 TTTCTCGGCTCAGGCCAGGCTGCACCCATTGGGGTGACCCAGCAGATGAGGCCCTGGAG 480  
QY 562 GTGGGGCTCCATGGAGTGGTGCCTTTCAGGTTTGAAGGAGCATTCGGTGCCTGGCGA 621  
Db 481 GTGGGGCTCCATGGAGTGGTGCCTTTCAGGTTTGAAGGAGCATTCGGTGCCTGGCGA 540  
QY 622 AACATCATCACTGGAACTCTCGGCTTCATCTCGGCAACGCCACCTGGTTCGTG 681  
Db 541 AACATCATCACTGGAACTCTCGGCTTCATCTCGGCAACGCCACCTGGTTCGTG 600  
QY 682 GTCCAGCTAACCATGAGCCCGAGGTCCACGAGCAACGCTGGCTGGTGCAGTTGGTG 741  
Db 601 GTCCAGCTAACCATGAGCCCGAGGTCCACGAGCAACGCTGGCTGGTGCAGTTGGTG 660  
QY 742 ACAGCCGCTTACAACTACTTCCATGTGACCAACTTCTTCTGGATGTTCCGCGAGGGCTGC 801  
Db 661 ACAGCCGCTTACAACTACTTCCATGTGACCAACTTCTTCTGGATGTTCCGCGAGGGCTGC 720  
QY 802 TACCTGCACAGCCATGCTGCTCACTACTCACTGACCGGCTGGCAATGATGTTTC 861  
Db 721 TACCTGCACAGCCATGCTGCTCACTACTCACTGACCGGCTGGCAATGATGTTTC 780  
QY 862 ATCTGCAATTGGCTGGGGTGTGCCCTTCCCATCATTTGTGSCCTGGSCCATTTGGGAAGCTG 921  
Db 781 ATCTGCAATTGGCTGGGGTGTGCCCTTCCCATCATTTGTGSCCTGGSCCATTTGGGAAGCTG 840  
QY 922 TACTACGACAAATGAGAAGTGTGCTGTTTGGCAAAAGGCTGGGGGTGTACACCGACTACATC 981  
Db 841 TACTACGACAAATGAGAAGTGTGCTGTTTGGCAAAAGGCTGGGGGTGTACACCGACTACATC 900  
QY 982 TACAGGGGCCCCATGATCCTGCTGCTGCTGATCAATTTCAATCTCTTTTCAACATGCTC 1041  
Db 901 TACAGGGGCCCCATGATCCTGCTGCTGCTGATCAATTTCAATCTCTTTTCAACATGCTC 960  
QY 1042 CGCATCCTCATGACCAAGCTCCGGGCATCCACCACTGTGAGACCATTCAGTACAGGAAG 1101  
Db 961 CGCATCCTCATGACCAAGCTCCGGGCATCCACCACTGTGAGACCATTCAGTACAGGAAG 1020  
QY 1102 GCTGTGAAAAGCCACTCTGCTGCTGCTGCCCTCTCGGGCATCACCTACATGCTGTTCTTC 1161  
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QY 1342 GCCCGTGCATGTCATCCCACTCCCAACCCGCTGTGAGTTCAGCATCAAGCAG 1401  
Db 1261 GCCCGTGCATGTCATCCCACTCCCAACCCGCTGTGAGTTCAGCATCAAGCAG 1320  
QY 1402 TCCACAGCAGTCTGA 1416

Db 1321 TCCACAGCAGTCTGA 1335

RESULT 11

US-08-110-286A-1

/ Sequence 1, Application US/08110286A

/ Patent No. 5728545

/ GENERAL INFORMATION:

/ APPLICANT: Perrin, Marilyn H.

/ APPLICANT: Chen, Ruoping

/ APPLICANT: Lewis, Kathy A.

/ APPLICANT: Vale Jr., Wylie W.

/ APPLICANT: Donaldson, Cynthia J.

/ TITLE OF INVENTION: CLONING AND RECOMBINANT PRODUCTION OF

/ NUMBER OF SEQUENCES: 6

/ CORRESPONDENCE ADDRESS:

/ ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark

/ STREET: 444 South Flower Street, Suite 2000

/ CITY: Los Angeles

/ STATE: CA

/ COUNTRY: USA

/ ZIP: 90071

/ COMPUTER READABLE FORM:

/ MEDIUM TYPE: Floppy disk

/ COMPUTER: IBM PC compatible

/ OPERATING SYSTEM: PC-DOS/MS-DOS

/ SOFTWARE: PatentIn Release #1.0, Version #1.25

/ CURRENT APPLICATION DATA:

/ APPLICATION NUMBER: US/08/110,286A

/ FILING DATE:

/ CLASSIFICATION: 435

/ PRIOR APPLICATION DATA:

/ APPLICATION NUMBER: US 08/079,320

/ FILING DATE: 18-JUN-1993

/ ATTORNEY/AGENT INFORMATION:

/ NAME: Reiter, Stephen E.

/ REGISTRATION NUMBER: 31,192

/ REFERENCE/DOCKET NUMBER: P41 9439

/ TELECOMMUNICATION INFORMATION:

/ TELEPHONE: 619-546-4737

/ TELEFAX: 619-546-9392

/ INFORMATION FOR SEQ ID NO: 1:

/ SEQUENCE CHARACTERISTICS:

/ LENGTH: 1380 base pairs

/ TYPE: nucleic acid

/ STRANDEDNESS: both

/ TOPOLOGY: both

/ MOLECULE TYPE: cDNA

/ FEATURE:

/ NAME/KEY: CDS

/ LOCATION: 82..1329 /product= "HUMAN PITUITARY

/ OTHER INFORMATION: CRF-RECEPTOR"

/ OTHER INFORMATION: /note= "This sequence is encoded by clone

/ OTHER INFORMATION: "CRF-R1".

US-08-110-286A-1

Query Match 81.1%; Score 1283; DB 2; Length 1380;

Best Local Similarity 94.1%; Pred. No. 4.8e-314;

Matches 1380; Conservative 0; Mismatches 0; Indels 87; Gaps 1;

QY 1 CGAGCCGCGAGCCGCGCGGTCTCTGGGATGTCGGTAGCACCAGGCGCATTCAGGAC 60

Db 1 CGAGCCGCGAGCCGCGCGGTCTCTGGGATGTCGGTAGCACCAGGCGCATTCAGGAC 60

QY 61 GGATAGCGAGCGAGCGAGGATGGAGGACCCCGAGCTCCGCTCTCGTCAAGGCGCCCT 120

Db 61 GGATAGCGAGCGAGCGAGGATGGAGGACCCCGAGCTCCGCTCTCGTCAAGGCGCCCT 120

QY 121 CTCCTCTGCGGGCTGAACCCCGTCTCTGCTCCCTCCAGACCAAGCACTGCGAGAGCCTG 180

Db 121 CTCCTCTGCGGGCTGAACCCCGTCTCTGCTCCCTCCAGACCAAGCACTGCGAGAGCCTG 180

QY 181 TCCCTGGCCAGCAACATCTCAGGACTGCAGTGCACCGCATCCGTGGACCTCAATTGGCACC 240

Db 181 TCCCTGGCCAGCAACATCTCAGGACTGCAGTGCACCGCATCCGTGGACCTCAATTGGCACC 240

QY 241 TGTGTGCCCCCGAGCCCTGCGGGGAGCTAGTGGTTCGGCCCTGCGCTGCTTTTCTAT 300

Db 241 TGTGTGCCCCCGAGCCCTGCGGGGAGCTAGTGGTTCGGCCCTGCGCTGCTTTTCTAT 300

QY 301 GGTGTCCGCTACAAATACCAAAATGGCTACCGGAGTGCCTGGCCAAATGGCAGCTGG 360

Db 301 GGTGTCCGCTACAAATACCAAAATGGCTACCGGAGTGCCTGGCCAAATGGCAGCTGG 360

QY 361 GCGCCCGCGGTAAATTTACTCCGAGTGCAGGAGATCTCAATGAGGAGAAAAAACAAG 420

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QY 421 GTGCACTACCATGTGCGAGTCAATCACTACCTGGGCCACTGTATATCTCCCTGGTGGCC 480

Db 421 GTGCACTACCATGTGCGAGTCAATCACTACCTGGGCCACTGTATATCTCCCTGGTGGCC 480

QY 481 CTCCTGGTGGCCCTTTGTCTCTTTCTGGGGCTCAGGCCAGGCTGCACCCATTGGGGTGAC 540

Db 481 CTCCTGGTGGCCCTTTGTCTCTTTCTGGGGCTC----- 513

QY 541 CAGGCAGATGGAGCCCTGGAGGTGGGGGCTCCATGGAGTGGTGGCCCAATTTCAGGTTTCCA 600

Db 541 ----- 513

QY 601 AGGAGCATCCGCTGCTGCGAAACATCATCCACTGGAACCTCATCTCCGCTTCATCTCTG 660

Db 601 AGGAGCATCCGCTGCTGCGAAACATCATCCACTGGAACCTCATCTCCGCTTCATCTCTG 660

QY 661 CGCAACGCCACCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720

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QY 721 GTGGGCTGCTGCAAGTGGTGTGACAGCGGCTTAACTTCTGCTGCTGCTGCTGCTGCTGCTG 780

Db 721 GTGGGCTGCTGCAAGTGGTGTGACAGCGGCTTAACTTCTGCTGCTGCTGCTGCTGCTGCTG 780

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QY 841 CGGCTGCGCAATGAGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900

Db 841 CGGCTGCGCAATGAGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900

QY 901 GCCTGGGCGCAATGGGAAGCTGTACTACGACAAATGAGAAGTGTGCTGCTGCTGCTGCTGCTG 960

Db 901 GCCTGGGCGCAATGGGAAGCTGTACTACGACAAATGAGAAGTGTGCTGCTGCTGCTGCTGCTG 960

QY 961 GGGGTGTACACCGACTACATCTACCGAGGCGCCATGATCCTGCTGCTGCTGCTGCTGCTGCTG 1020

Db 961 GGGGTGTACACCGACTACATCTACCGAGGCGCCATGATCCTGCTGCTGCTGCTGCTGCTGCTG 1020

QY 1021 ATCTTCTTTTCAACATCGTCCGATCTCATGACCAAGCTCGGGCATCCACCATGCTCT 1080

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QY 1081 GAGACCATTCAGTACAGGAAGCTGTGAAAGGCACCTCTGCTGCTGCTGCTGCTGCTGCTGCTG 1140

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QY 1141 ATCACCCTACATGCTGTTCTTCTGCTCAATCCCGGGAGAGTGAAGTCTCCCGGGTCTGCTTTC 1200

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QY 1201 ATCTACTTCACTCTTCTTCTGGAATCTTCCAGGGCTTCTTGTGCTGCTGCTGCTGCTGCTGCTG 1260

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QY 1261 TTCCTCAATAGTGGAGTCCGTTCTGCCATCCGGAAGAGGTGGCACCGGTGGCAGGACAAG 1320  
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QY 1321 CACTCCATCCGTCGCCGAGTGGCCCGTGCATATCCCACTCCCAACCCCGTGC 1380  
DB 1234 CACTCGATCCGTCGCCGAGTGGCCCGTGCATATCCCACTCCCAACCCCGTGC 1293  
QY 1381 AGCTTTCAAGCATCAAGCATGTCACAGCATGTCAGCTGGCAGGTGATGAGAGAGCCCC 1440  
DB 1294 AGCTTTCAAGCATCAAGCATGTCACAGCATGTCAGCTGGCAGGTGATGAGAGAGCCCC 1353  
QY 1441 CAAAGAGCTGTGCTGGGGGATGAG 1467  
DB 1354 CAAAGAGCTGTGCTGGGGGATGAG 1380

RESULT 12  
US-09-799-978-3  
; Sequence 3, Application US/09799978  
; Patent No. 6670140  
; GENERAL INFORMATION:  
; APPLICANT: The Procter & Gamble Company  
; APPLICANT: Isfort, Robert  
; APPLICANT: Sheldon, Russell  
; TITLE OF INVENTION: Methods for Identifying Compounds for Regulating Muscle Mass or  
; FILE REFERENCE: 8448  
; CURRENT APPLICATION NUMBER: US/09/799, 978  
; CURRENT FILING DATE: 2001-03-06  
; NUMBER OF SEQ ID NOS: 44  
; SOFTWARE: Patent in version 3.0  
; SEQ ID NO 3  
; LENGTH: 1285  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (38)..(1285)  
US-09-799-978-3

Query Match 75.1%; Score 1188; DB 3; Length 1285;  
Best Local Similarity 93.7%; Pred. No. 4.3e-290;  
Matches 1285; Conservative 0; Mismatches 0; Indels 87; Gaps 1;

QY 45 CCGGGCATTCAGAGCGTAGCCGAGCGAGCCCGAGAGTGGAGGGCACCCGAGCTCCG 104  
DB 1 CCGGGCATTCAGAGCGTAGCCGAGCGAGCCCGAGAGTGGAGGGCACCCGAGCTCCG 60  
QY 105 TCTCGTCAAGGCCCTTCTCCTTCTGGGGCTGAAACCCCGTCTCTGCTCCCTCCAGGACCA 164  
DB 61 TCTCGTCAAGGCCCTTCTCCTTCTGGGGCTGAAACCCCGTCTCTGCTCCCTCCAGGACCA 120  
QY 165 GCATCGGAGAGCTCTCCTGCGCAGACATCTCAGGACTCAGTGGCAAGCATCCGT 224  
DB 121 GCATCGGAGAGCTCTCCTGCGCAGACATCTCAGGACTCAGTGGCAAGCATCCGT 180  
QY 225 GGAACCTCATTTGGCAGCTGTGCGCCCGCAGCCCTGGGGGAGTGTGTTCCGGCCCTG 284  
DB 181 GGAACCTCATTTGGCAGCTGTGCGCCCGCAGCCCTGGGGGAGTGTGTTCCGGCCCTG 240  
QY 285 CCTGCTCTTTTCTATGTTGTCGCTACATACCAACAAATGGTGTACCGGAGTGCCT 344  
DB 241 CCTGCTCTTTTCTATGTTGTCGCTACATACCAACAAATGGTGTACCGGAGTGCCT 300  
QY 345 GGCATGCGAGCTGTGGCCCGCCCGGTGATTAATCTCGAGTGGCAGGAGTCTCAATGA 404  
DB 301 GGCATGCGAGCTGTGGCCCGCCCGGTGATTAATCTCGAGTGGCAGGAGTCTCAATGA 360  
QY 405 GGAGAAAAAAGCAAGGTGCACTACCATGTGCGAGTCAATCACTACCTGCGGCCACTG 464  
DB 361 GGAGAAAAAAGCAAGGTGCACTACCATGTGCGAGTCAATCACTACCTGCGGCCACTG 420

RESULT 13  
US-09-826-509-482  
; Sequence 482, Application US/09826509  
; Patent No. 6806054  
; GENERAL INFORMATION:  
; APPLICANT: Lehmann-Bruinsma, Karin  
; APPLICANT: Liew, Chen W.  
; APPLICANT: Lin, I-Lin

QY 465 TATCTCCTCTGGTGGCCCTCTCTGGTGGCCCTTGTCTCTCTCTCTCTGGCGCTCAGGCCAGGCTG 524  
DB 421 TATCTCCTCTGGTGGCCCTCTCTGGTGGCCCTTGTCTCTCTCTCTCTGGCGCTCAGGCCAGGCTG 469  
QY 525 CACCCATTGGGGGTGACACAGGAGATGGAGCCCTGGAGGTGGGGGCTCCATGGAGTGGTGC 584  
DB 470 ----- 469  
QY 585 CCCATTTCAGGTTGGAAGAGCATCCGGTGCCTGCGAAACATCATCATCTGGAACCTCAT 644  
DB 470 -----AGGAGCATCCGGTGCCTGCGAAACATCATCATCTGGAACCTCAT 513  
QY 645 CTCGGCTTCATCTCGCGCAACGCGCACCTGGTTCTGCTGCTCCAGCTAACCATAGAGCCCGCA 704  
DB 514 CTCGGCTTCATCTCGCGCAACGCGCACCTGGTTCTGCTGCTCCAGCTAACCATAGAGCCCGCA 573  
QY 705 GGTCCACAGAGCAACGCTGGGGTGTGTCAGAGTGTGTCAGAGCCGCTTACAACTACTTTCCA 764  
DB 574 GGTCCACAGAGCAACGCTGGGGTGTGTCAGAGTGTGTCAGAGCCGCTTACAACTACTTTCCA 633  
QY 765 TGTGACCAACTTCTCTGATGTTTCGGGAGGCTGCTACTGTCACACAGCCATCTGCTGT 824  
DB 634 TGTGACCAACTTCTCTGATGTTTCGGGAGGCTGCTACTGTCACACAGCCATCTGCTGT 693  
QY 825 CACTACTCCACTGACCGGCTGGCCATTTGGGAAGTGTCTCATCTGCTATGCTGGTGGGTGTC 884  
DB 694 CACTACTCCACTGACCGGCTGGCCATTTGGGAAGTGTCTCATCTGCTATGCTGGTGGGTGTC 753  
QY 885 CTTTCCCATCATTTGTGGCTGGCCATTTGGGAAGTGTCTCATCTGCTATGCTGGTGGGTGTC 944  
DB 754 CTTTCCCATCATTTGTGGCTGGCCATTTGGGAAGTGTCTCATCTGCTATGCTGGTGGGTGTC 813  
QY 945 GTTTGGCAAAAGGCTGGGGTGTACACCGACTATACCTACAGGGGCCCATGATCTCTGCT 1004  
DB 814 GTTTGGCAAAAGGCTGGGGTGTACACCGACTATACCTACAGGGGCCCATGATCTCTGCT 873  
QY 1005 CTGCTGATCAATTTTCATCTCTCTTTTCAACATCTGTCGCTCATCTGATGACCAAGCTCCG 1064  
DB 874 CTGCTGATCAATTTTCATCTCTCTTTTCAACATCTGTCGCTCATCTGATGACCAAGCTCCG 933  
QY 1065 GGCATCCACAGCTCTGAGACCAATTCAGTACAGGAAGGCTGTGAAAGCCACTCTGCTGT 1124  
DB 934 GGCATCCACAGCTCTGAGACCAATTCAGTACAGGAAGGCTGTGAAAGCCACTCTGCTGT 993  
QY 1125 GTGCCCCCTCTGGGCAATCACTATGCTGTTCTTCTGTCATCTCCGGGGAGGATGAGGT 1184  
DB 994 GTGCCCCCTCTGGGCAATCACTATGCTGTTCTTCTGTCATCTCCGGGGAGGATGAGGT 1053  
QY 1185 CTCGGGCTGGTCTTTCATCTTCACTTCACTCTCTTCTGGAATCCTTCCAGGGCTTCTTGT 1244  
DB 1054 CTCGGGCTGGTCTTTCATCTTCACTTCACTCTTCTGGAATCCTTCCAGGGCTTCTTGT 1113  
QY 1245 GTCTGTGTTCTACTGTTTCTCAATAGTGAAGTCCGTTCTGCTCATCCGGAAGAGGTGGCA 1304  
DB 1114 GTCTGTGTTCTACTGTTTCTCAATAGTGAAGTCCGTTCTGCTCATCCGGAAGAGGTGGCA 1173  
QY 1305 CCGGTGGAGGACAAGCACTCGATCCGTCGCGAGTGGCCCGTGCATATGCTCCATCCCCAC 1364  
DB 1174 CCGGTGGAGGACAAGCACTCGATCCGTCGCGAGTGGCCCGTGCATATGCTCCATCCCCAC 1233  
QY 1365 CTCGCCAACCGGTGTCAGCTTTTTCAGATCAAGCATCAAGCATCCAGAGTCTGA 1416  
DB 1234 CTCGCCAACCGGTGTCAGCTTTTTCAGATCAAGCATCAAGCATCCAGAGTCTGA 1285

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; TITLE OF INVENTION: No. 6806054-Endogenous, Constitutively Activated Known G
; TITLE OF INVENTION: Protein-Coupled Receptors
; FILE REFERENCE: AREN-207
; CURRENT APPLICATION NUMBER: US/09/826,509
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/195,747
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 589
; SOFTWARE: PatentIn Version 2.1
; SEQ ID NO 482
; LENGTH: 1248
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-826-509-482

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Query Match 72.7%; Score 1149.4; DB 3; Length 1248;  
Best Local Similarity 93.4%; Pred. NO. 2.4e-280;  
Matches 1247; Conservative 0; Mismatches 1; Indels 87;

Qy	82	ATGGGAGGGCACCCGCACTCGTCTCGTCTCAAGGCCCCCTTCTCTTCTGGGGCTGAACCCC	141
Db	1	ATGGGAGGGCACCCGCACTCGTCTCGTCAAGGCCCTTCTCTTCTGGGGCTGAACCCC	60
Qy	142	GTCTCTGCCCTCCCTCCAGGACCGACACTCGGAGAGCGCTGCCCTGGCCGACGAACTCTCA	201
Db	61	GTCTCTGCCTCCCTCCAGGACGAGCACTCGGAGAGCGCTGCCCTGGCCGACGAACTCTCA	120
Qy	202	GGACTGCAGTGCAACGCACTCCGTGGAACCTCATTTGGCACTGTGTGCCCGCCGACGCCCTGGC	261
Db	121	GGACTGCAGTGCAACGCACTCCGTGGAACCTCATTTGGCACTGTGTGCCCGCCGACGCCCTGGC	180
Qy	262	GGGCACTAGTGGTTTCGGCCCTCGCCCTCTTTTCTATGTGTCCGTACAAATACCA	321
Db	181	GGGCACTAGTGGTTTCGGCCCTCGCCCTCTTTTCTATGTGTCCGTACAAATACCA	240
Qy	322	AACAAATGGCTACCGGAGTGGCTGTGCCCAATGGCAGCTGGCGCCGCGGTGAATTTACTCC	381
Db	241	AACAAATGGCTACCGGAGTGGCTGTGCCCAATGGCAGCTGGCGCCGCGGTGAATTTACTCC	300
Qy	382	GAGTGCCAGGAGATCCTCAATGAGGAGAAAAAAGCAAGGTGCACCTACCATGTCCGACGTC	441
Db	301	GAGTGCCAGGAGATCCTCAATGAGGAGAAAAAAGCAAGGTGCACCTACCATGTCCGACGTC	360
Qy	442	ATCATCAACTACTCTGGGCCACTGTATATCTCCCTGTGTGGCCCTCTGGTGCCCTTTGTCTTC	501
Db	361	ATCATCAACTACTCTGGGCCACTGTATATCTCCCTGTGTGGCCCTCTGGTGCCCTTTGTCTTC	420
Qy	502	TTTCTGGGCTCAGGCCAGGCTGCACCCATTGGGGTGACAGGCAGATGGAGCCCTGGAG	561
Db	421	TTTCTGGGCTC-----TTTCTGGGCTC-----	432
Qy	562	GTGGGGGTCCATGGAGTGTGGTCCCACTTCAGGTTTCGAAGAGCATCCGGTGCCCTGGCA	621
Db	433	-----AGAGGATCCGGTGCCCTGGCA	453
Qy	622	AACATCATPCCACTGAAACCTCATCTCCGCTTCATCTCTGCGCAACGCCCACTGTGTCGTG	681
Db	454	AACATCATPCCACTGAAACCTCATCTCCGCTTCATCTCTGCGCAACGCCCACTGTGTCGTG	513
Qy	682	GTCCAGCTTAACATGAGCCCGAGGTCCACCGAGCAACGTTGGCTGTGTGCAGTTGGTG	741
Db	514	GTCCAGCTTAACATGAGCCCGAGGTCCACCGAGCAACGTTGGCTGTGTGCAGTTGGTG	573
Qy	742	ACAGCGGCTACAACTACTTCCATGTGACCAACTTCTCTGATGTTTGGCGAGGCGCTGC	801
Db	574	ACAGCGGCTACAACTACTTCCATGTGACCAACTTCTCTGATGTTTGGCGAGGCGCTGC	633
Qy	802	TACCTGCACACAGCCATCGTGTCACTTCACTGACCGGCTCGCAAAATGGAGTTTC	861
Db	634	TACCTGCACACAGCCATCGTGTCACTTCACTGACCGGCTCGCAAAATGGAGTTTC	693

## RESIT.T 14

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US-09-799-978-7
; Sequence 7, Application US/09799978
; Patent No. 6670140
; GENERAL INFORMATION:
; APPLICANT: The Procter & Gamble C
; APPLICANT: Isfort, Robert
; APPLICANT: Sheldon, Russell
; TITLE OF INVENTION: Methods for
; TITLE OF INVENTION: Function Usin
; FILE REFERENCE: 8448
; CURRENT APPLICATION NUMBER: US/09/
; CURRENT FILING DATE: 2001-03-06
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 1206
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1206)
US-09-799-978-7

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Query Match	66.8%	Score 1057	DB 3	Length 1206
Best Local Similarity	90.3%	Pred. No. 5.1e-257		
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Db	1	ATGGGAGGGGCAACCGCAGCTCCGTCTCGTCAAGGCCCTTCTCTCTTGGGGCTGAACCCC	60	

142 GTCTCTGCTCCCTCCAGGACGAGCTGCGAGAGCTGTCCCTGGCCAGCAATCTCA 201  
Db  
61 GTCTCTGCTCCCTCCAGGACGAGCTGCGAGAGCTGTCCCTGGCCAGCAATCTCA 120  
QY  
202 GGAATGAGTGCACGATCCGCTGAGCTCAATGAGCACTGCTGGCCCGCCAGCTTCG 261  
Db  
121 GGAATGAGTGCACGATCCGCTGAGCTCAATGAGCACTGCTGGCCCGCCAGCTTCG 180  
QY  
262 GGGAGCTAGTGGTTCGGCCCTGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 321  
Db  
181 GGGAGCTAGTGGTTCGGCCCTGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 240  
QY  
322 AACATGGCTACCGGAGTGCCTGGCCAAATGGAGCTGGCCCGCCGCTGAATTAATCC 381  
Db  
241 AACATGGCTACCGGAGTGCCTGGCCAAATGGAGCTGGCCCGCCGCTGAATTAATCC 300  
QY  
382 GAGTGGCAGGAGATCTCAATGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 441  
Db  
301 GAGTGGCAGGAGATCTCAATGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360  
QY  
442 ATCATCAATACCTGGGCACTGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 501  
Db  
361 ATCATCAATACCTGGGCACTGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 420  
QY  
502 TTTCTGGGCTCAGGCCAGGCTGCACCCATGGGCTGACCCAGGAGATGAGCCCTGGAG 561  
Db  
421 TTTCTGGGCTC----- 432  
QY  
562 GTGGGGCTCCATGGAGTGTGGCCCAATTTTCAGGTTGGAAGGAGATCCGGTGCCTGCGA 621  
Db  
433 -----AGGAGATCCGGTGCCTGCGA 453  
QY  
622 AACATCACTGGAACCTCATCTCGCTTCACTGCGCAACGCACTGGTTCGTG 681  
Db  
454 AACATCACTGGAACCTCATCTCGCTTCACTGCGCAACGCACTGGTTCGTG 513  
QY  
682 GTCCAGTCAACATGAGCCCGAGGCTCCACGAGCAACGCTGGCTGGTTCAGGTTGGT 741  
Db  
514 GTCCAGTCAACATGAGCCCGAGGCTCCACGAGCAACGCTGGCTGGTTCAGGTTGGT 573  
QY  
742 ACAGCGCTTACAACTACTTCCATGTGACCACTTCTTCTGATGTTGCGCGAGGCTGC 801  
Db  
574 ACAGCGCTTACAACTACTTCCATGTGACCACTTCTTCTGATGTTGCGCGAGGCTGC 633  
QY  
802 TACTGACACAGCCATCTGCTCCTCACTACTCACTGACCGGCTGGCAATGATGTTTC 861  
Db  
634 TACTGACACAGCCATCTGCTCCTCACTACTCACTGACCGGCTGGCAATGATGTTTC 693  
QY  
862 ATCTGCAATGGCTGGGCTGCTGCTTCCCATCACTGCTGGCTGGCCATTTGGAGCTG 921  
Db  
694 ATCTGCAATGGCTGGGCTGCTGCTTCCCATCACTGCTGGCTGGCCATTTGGAGCTG 753  
QY  
922 TACTGACACAAATGAGAGTCTGTTTGGCAAGGCTGGGCTGTACCGACTATCATC 981  
Db  
754 TACTGACACAAATGAGAGTCTGTTTGGCAAGGCTGGGCTGTACCGACTATCATC 813  
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982 TACCAGGGCCCCATGATCTGCTGCTGCTGATCAATTTCTCTCTTTTCAACATGCTC 1041  
Db  
814 TACCAGGGCCCCATGATCTGCTGCTGCTGATCAATTTCTCTCTTTTCAACATGCTC 873  
QY  
1042 CGCATCTCATGACCAAGCTCCGGGCAATCAACAGCTGTAGAGCAATTCAGTACAGGA 1101  
Db  
874 CGCATCTCATGACCAAGCTCCGGGCAATCAACAGCTGTAGAGCAATTCAGTACAGGA 933  
QY  
1102 GCTGTGAAGCCACTCTGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1161  
Db  
934 GCTGTGAAGCCACTCTGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 993  
QY  
1162 GTCAATCCCGGGAGGATGAGGCTCTCCCGGCTGCTTCTCACTTCACTTCACTTCTCT 1221  
Db  
994 GTCAATCCCGGGAGGATGAGGCTCTCCCGGCTGCTTCTCACTTCACTTCACTTCTCT 1053  
QY  
1222 GAATCTCTCCAGGGCTTCTTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1281

Db 1054 GAACTCTTCC-----AGGTCCGT 1071  
QY 1282 TCTGCCATCCGGAAGAGTGGCAACCGTGGCAGCAAGCACTCGATCCGTGCCAGTG 1341  
Db 1072 TCTGCCATCCGGAAGAGTGGCAACCGTGGCAGCAAGCACTCGATCCGTGCCAGTG 1131  
QY 1342 GCGCGTGCATGCTCCATCCCACTCCCAACCGTGTGAGCTTTCACAGCATCAAGCAG 1401  
Db 1132 GCGCGTGCATGCTCCATCCCACTCCCAACCGTGTGAGCTTTCACAGCATCAAGCAG 1191  
QY 1402 TCCACAGCATGTGA 1416  
Db 1192 TCCACAGCATGTGA 1206  
RESULT 15  
US-08-482-746-5  
; Sequence 5, Application US/08482746B  
; Patent No. 6399315  
; GENERAL INFORMATION:  
; APPLICANT: Perrin, Marilyn H.  
; APPLICANT: Chen, Ruoping  
; APPLICANT: Lewis, Kathy A.  
; APPLICANT: Vale Jr., Wylie W.  
; APPLICANT: Donaldson, Cynthia J.  
; APPLICANT: Sawchenko, Paul  
; TITLE OF INVENTION: Cloning and Recombinant Production of  
; FILE REFERENCE: P41-90002  
; CURRENT APPLICATION NUMBER: US/08/482,746B  
; CURRENT FILING DATE: 1995-06-07  
; EARLIER APPLICATION NUMBER: US 08/374,009  
; EARLIER FILING DATE: 1995-01-17  
; EARLIER APPLICATION NUMBER: US 08/353,537  
; EARLIER FILING DATE: 1994-12-09  
; EARLIER APPLICATION NUMBER: PCT/US94/05908  
; EARLIER FILING DATE: 1994-05-25  
; EARLIER APPLICATION NUMBER: US 08/110,286  
; EARLIER FILING DATE: 1993-08-23  
; EARLIER APPLICATION NUMBER: US 08/079,320  
; EARLIER FILING DATE: 1993-06-18  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 5  
; LENGTH: 1411  
; TYPE: DNA  
; ORGANISM: Rattus  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (80)...(1324)  
US-08-482-746-5  
Query Match 65.4%; Score 1035.2; DB 3; Length 1411;  
Best Local Similarity 83.8%; Pred. No. 1.7e-251;  
Matches 1258; Conservative 0; Mismatches 153; Indels 91; Gaps 4;  
QY 3 AGCCCGCAGCGCCCGCCGCTTCTCTGGGATGTCCTGAGACCCCGGCAATTCAGGACG 62  
Db 1 AGACCGCAGCGCCCGCCGCTTCTGGATGTCGAGCGATCCAGGATCCAGGACG 60  
QY 63 TAGCCGAGGAGCCCGGAGATGGAGGCAACCGAGCTCCGTCCTGTCAGGCGCTTCT 122  
Db 61 TGACGAGGAGCCCGGAGATGGAGCGCCCGCAGCTCCGCTCGTGAAGGCCCTTCT 120  
QY 123 CCTTCTGGGCTGAACCCCGCTCTCTCCCTCCCTCCAGGACAGCACTGCGAGAGCTGTC 182  
Db 121 CCTTCTGGGCTGAACCCCTGTGTCCACCTCCCTTCAGGATCAGGCTGTGAGAACCTGTC 180  
QY 183 CTTGGCAGCAACATCTCAGAGCTGCAAGTGCACGATCCGTGGAGCTCATTTGGCACCTG 242  
Db 181 CTTGACCAACGATGTTTCTGGCTGTCAGTGCATGATCCGTGACCTCATTTGGCACCTG 240

Qy	243	CTGGCCCGGACGCCCTCTGGGGGAGCTAGTGTGTTCGGCCCTCGCCCTGCTTCTTCTA	302
Db	241	CTGGCCCGGAGCCCTCGGGGCCAATGTGTGTTCGGACCCCTGGCCCTTCTTCTACGG	300
Qy	303	TGTCGGCTTACAATACCAACAACAACTGCTACCGGAGTGCTCGCCCAATGGCAGCTGGGC	362
Db	301	TGTCCGCTTACAACAACGACAAACAATAGTCTACCGGAGTGCTCGCCCAACGGCAGCTGGGC	360
Qy	363	CGCCCGGTGAATTTACTCCGAGTGCCAGGAGATCCTCAATGAGGAGAAAAAGCAAGGT	422
Db	361	AGCCCGGTGAATTTATTTCTGAGTGCCAGAGATTCTCAAAGAGAGAGAGCAAGT	420
Qy	423	GCACATCATGTCCGAGTCAATCAATCACTCTGGGCCACTGTATCTCCCTGTGGCCCT	482
Db	421	ACACTAGCATGTTGAGTCAATCAATCACTCGGTCACTGCAATCTCCCTGTGGTAGCCCT	480
Qy	483	CCTGGTGGCCCTTTGTGCTCTTTCTGGGCTCAGGCCAGGCTGCACCAATTTGGGGTGACCA	542
Db	481	CCTGGTGGCCCTTTGTGCTCTTTCTTGGGCTC-----	511
Qy	543	GGCAGATGGAGCCCTGGAGGTGGGGGCTCCATGAGTGTGTGCCCAATTCAGGTTTCGAAG	602
Db	512	-----AG	513
Qy	603	GAGCATCGGTGCTCTGGAAACATCATCTCACTGGAACTCATCTCGCCCTCAATCTGTGG	662
Db	514	GAGCATCGGTGCTCTGGAAACATCATCTCACTGGAACTCATCTCGGCTTTCATCTCTACG	573
Qy	663	CAACGCCACCTGGTTCGTGTCCAGCTTAAACCATGAGCCCCGAGGTCCACACAGCAACGT	722
Db	574	CAACGCCACCTGGTTCGTGTCCAGCTTCAACGTGAGCCCCGAGGTGCACACAGCAACATGT	633
Qy	723	GGGCTGTGTGAGGTTGGTGAACAGCCGCTTACAACTTTCATGTGACCAACTTCTTCTG	782
Db	634	GGCCTGTGTGAGGTTGGTGAACAGCCGCTTACAACTTTCATGTGACCAACTTCTTCTG	693
Qy	783	GATGTTCCGGAGGGCTGCTACTGCAACAGCCCATCGTGCTCACTTCCACTGACCG	842
Db	694	GATGTTCCGGTGAAGGCTGCTACTGCAACAGCCCATTTGTGCTCACTCCACCGACCG	753
Qy	843	GCTCGGCAATAGATGTTTCATCTGCATTTGGTGGGGTGTGCCCTTCCCATCATTTGTGGC	902
Db	754	TCTCGCAAGTGGATGTTTCGTCTGCATTTGGCTGGGGTGTACCTTTCCCCCATCATTTGGGC	813
Qy	903	CTGGGCCAATGGGAAGCTGTACTACGACAATGAGAAGTGTCTGGTTTGGCAAAAGGCCCTGG	962
Db	814	TTGGGCCAATGGGAAGCTGTCACTACGACAATGAAGAAGTGTGTGTTTGGCAAAAGTCTCTGG	873
Qy	963	GGTGTAACCGACTATCACTACAGGGCCCCATGATCCTGGTCTGTGTGATCAATTTTCAT	1022
Db	874	GGTATACACTGACTATCATCTACCAAGGGCCCCATGATCCTGGTCTGTGTCAACTTTAT	933
Qy	1023	CTTCTCTTTTCAACATGCTCGCATCTCATGACCAAGCTCGGGGCATCCACCACTCTGA	1082
Db	934	CTTTCTCTTTCAACATTTGTCCGCATCTCATGACCAAACTCCGGGCAATCCACTACATCTGA	993
Qy	1083	GACCAATTCAGTACAGGAAGGCTGTGAAGCCACATCTGTGTGTGCTGCCCTCTGGGGCAT	1142
Db	994	GACCAATTCAGTACAGGAAGGCTGTGAAGGCCACATCTGTGTGTCTCTGCCCTTCTGGGCAT	1053
Qy	1143	CACCTACATGCTGTTCTTTCGTCAAATCCCGGGGAGGATGAGGTCTCCCGGGTCTTTCAT	1202
Db	1054	CACCTACATGTTGTTCTTTCTGTCACACCTGGAGAGGACGAGGTCTCCAGGGTCTGTTTCAT	1113
Qy	1203	CTACTTCAACTCTCTCTGNAATCTTTCAGGGCTTCTTTGTGTCTGTGTCTACTGTGTTT	1262
Db	1114	CTACTTCAACTCTTTTCTCGGAGTCTTTTTCAGGGGCTTCTTTGTGTCTGTGTCTACTGTGTT	1173
Qy	1263	CCTCAATAGTGAAGTTCGTTCTGTCATCCGGAAGAGGTGGCACCCTGGTGGCAGCAAGCA	1322
Db	1174	TCTGNAACAGTGAAGTTCGCTCCGCTATCCGGAAGAGGTGGCGTGGTGGCAGCAAGCA	1233
Qy	1323	CTCGATCCGTGCCGAGTGGCCCGTGCAATGTCCATCCCACTCCCGCAACCCGTGTCTAG	1382







Db 287 GGACGGCTGGGAGAGCCCGGACCCGGAAGGTCCCTACTCTCTGCAACAGACCTT 346  
Qy 225 GGAACCTCATTTGGGCACTGCTGGCCCCGACGACCTGGGGGAGAGTGTGTCGGGCTG 284  
Db 347 GGACCAATCGGACCTGCTGGCCCCGAGAGCGGCTGGAGCCCTAGTGAGAGACCATG 406  
Qy 285 CCCTGCTTTTCTATGGTGTGCGCTACATACCAACAAAGTGTACCGGAGTGCCT 344  
Db 407 CCCGAAATCTTCAACGGCATCAAGTATACACGACCCGGAATGCCCTACAGAAATGCCT 466  
Qy 345 GGCAATGGCAGCTGGGCGCCCGCGCTGAATTAATCTCGAGTGGCAGGAGATCCTCAATG- 403  
Db 467 GGAGATGGACCTGGGCTCAAGGATCACTACTACACTGTGNAACCATTTGGATGA 526  
Qy 404 --AGGAGAAAAAGCAAGGTGCACTACCATGTCGAGTGCATCATCACTACTCTGGGCCA 461  
Db 527 CAAGCAGAGAAATGATGACCTGCAATACCGAATCGCCCTCATCACTACCTGGGCCA 586  
Qy 462 CTGTATCTCCCTGCTGGCCCTCTGGTGGCTTTGTCCTCTTTCTGGGCTCAGGCCAGG 521  
Db 587 CTGTGTTTCGTGGTGGCCCTGGTGGCTGCTTTCTCTGCTTTTCTCT----- 631  
Qy 522 CTGCACCCATTGGGSGTGACCAAGCAGATGAGGCCCTGGAGGTGGGGCTCCATGAGTGG 581  
Db 632 ----- 631  
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Qy 642 CATCTCGCCTTATCTCTGGCAACGCCACCTGGTTCGTGGTCCAGTAACTACCATGAGCC 701  
Db 680 CATCACACCTTATCTCTGAGAAATCACTGCTGGTTCCTCTGCACT---CATGACCA 736  
Qy 702 CGAGGTCCACACAGCAACCTGGGCTGGTGCAGGTGGTGCACAGCCGCTTACAACTACTT 761  
Db 737 CGAAGTGCAAGGGCAATGAGTCTGGTCCGCTGGCTCACCACCATATTCAGTACTT 796  
Qy 762 CCATGTGACCAACTTTCTTGTGAGTTTGGCGAGGGCTGTACTGTGCACACGCCATCGT 821  
Db 797 TGTGGTCAACCACTTCTTCTGGATGTTGTGGAAGGCTGTACTGTGCACACGCCATCGT 856  
Qy 822 GCTCACTACTCCACTGACCGGCTGGCAATGAGTGTTCATCTGCACTGGCTGGGGTGT 881  
Db 857 CATGACGTACTCACGAGCATCTGGCAAGTGGCTTCTCTTCAATGGATGGTGCAT 916  
Qy 882 GCCCTTCCCATCATTTGTGGCCTGGGCAATTGGAGCTGTACTACGACAAATGAGAAGTG 941  
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Qy 1002 GGTCTGCTGATCAATTTTCACTTCTTTTCAACATGCTGGCATCTCATGACCAAGCT 1061  
Db 1037 CGTGTCTCTCATCAATTTTGTGTTCTGTTTCAACATGCTCAGGATCTGTATGACAAACT 1096  
Qy 1062 CCGGGATCCACACAGCTCTGAGACCATTCAGTACAGGAGGCTGTGAAGCCACTCTGTT 1121  
Db 1097 GCGAGCTCCACACATCCGAGACCATTCAGTACAGGAGGAGTGAAGGCCACCTGTT 1156  
Qy 1122 GCTGCTGCCCTCTCTGGGCACTACCTACATGCTGTTCTTCTGTCATCCCGGGGAGGATGA 1181  
Db 1157 CCTCTCTCCCTCTGTGGGCATCACTTACATGCTCTTCTTGTCAATCTCTGGAGGACGA 1216  
Qy 1182 GGTCTCCGGGTGCTCTTCACTTCACTTCACTCTCTCTGCTGGAATCTCTTCAGGGCTTCTT 1241  
Db 1217 CTGTGACAGATTTGTCTACTTACTTCACTCTTCTCTGAGTCTCTTTCAGGGTTCTT 1276  
Qy 1242 TGTGCTGTGTTCTACTGTTTCTCAATAGTGAAGTCCGTTCTGCAATCCGGAAGGTTG 1301  
Db 1277 TGTGTCGTTTCTACTGCTTCTCAATGAGAGGTTGCGCTCCGCTGTGAAGGCGGTG 1336

Qy 1302 GCACCGGTGGCAGGACAAGCACTCGATCCGTGCCCGAGTGGCCCGTGCATGTCCATCCC 1361  
Db 1337 GCACCGTTGGCAGGACCACCAACGCTCCGAGTGCCTGTGGCCCCGGGCCATGTCCATTC 1396  
Qy 1362 CACTCCCCAACCCGCTGTCAGCTTTTCCACAGCACTCAAGCAGTCCACAGCAGTCTTGAGC 1418  
Db 1397 CACATGCCCAACCAAGATCAGCTTCCACAGCATCAAGCAGACAGCTGCCGTGTGATC 1453

## RESULT 3

US-11-136-527-6936  
; Sequence 6936, Application US/111136527  
; Publication No. US20050287570A1  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: Mounts, William M  
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes  
; FILE REFERENCE: 031896-041000 (AM101086)  
; CURRENT APPLICATION NUMBER: US/11/136,527  
; CURRENT FILING DATE: 2005-05-25  
; PRIOR APPLICATION NUMBER: US 60/574,294  
; PRIOR FILING DATE: 2005-05-26  
; NUMBER OF SEQ ID NOS: 362830  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 6936  
; LENGTH: 600  
; TYPE: DNA  
; ORGANISM: Rattus norvegicus  
US-11-136-527-6936

Query Match 29.3%; Score 464.2; DB 12; Length 600;  
Best Local Similarity 87.4%; Pred. No. 3.3e-107;  
Matches 527; Conservative 12; Mismatches 60; Indels 4; Gaps 3;

Qy 891 CATCATTTGGCTGGCCCATTTGGGAAGCTGTACTACGAACTAGAGAAGTGTGTTGG 950  
Db 1 CATCATTTGGCTGGCCCATTTGGGAAGCTGTACTACGAACTAGAGAAGTGTGTTGG 60  
Qy 951 CAAAGCCCTGGGGTGTACACCGACTACATCTACAGGGGCCCATGATCTGCTCTGCT 1010  
Db 61 CAAAGCCCTGGGGTGTACATGACTACATCTACAGGGGCCCATGATCTGCTCTGCT 120  
Qy 1011 GATCAATTTCACTTCTCTTTTCAACATCGTCCGATCTCATGACCAAGCTCGGGATC 1070  
Db 121 GATCAATTTTATCTTCTTCTTCAACATTTGTCGATCTCATGACCAAACTCGGGATC 180  
Qy 1071 CACCAGCTCTGAGACCACTTACGATACAGGAAGGCTGTGAAGCCACTCTGCTGCTGCC 1130  
Db 181 CACTACATCTGAGACCACTTCACTGAGGAAGGCTGTGAAGGCCACTCTGCTGCTGCC 240  
Qy 1131 CCTCTGGGCATCACCCTACATGCTGTTCTTCTGTCATCTCCGGGAGGATGAGGTCTCCCG 1190  
Db 241 CCTCTGGGCATCACCCTACATGTTGTTCTTCTGTCACCTCTGGAGAGGAGGTCTCCAG 300  
Qy 1191 GGTGCTCTTCACTACTCTCAATCTCTTCTGGAATCTCTTCAGGGCTTCTTGTGCTGT 1250  
Db 301 GGTGCTCTTCACTACTCTCAACTCTTCTTCTGAGTCTCTTTCAGGRCCTCTTGTGCTGT 360  
Qy 1251 GTTCTACTGTTTCTCTCAATAGTGAAGTCCGTTCTGTCATCTCCGGAAGGTTGGCACCGGTG 1310  
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Db 421 GCAGGACAAGCACTCCATCAGAGCCGAGTGGGCCGAGTATGTTCATCTCCACCTCCCT 480  
Qy 1371 AACCCGCTGTCAGCTTTTACAGCATCAAGCAGTCCACAGCAGTCTGAGCTGAGGTCATG 1430  
Db 481 GACCAGAGTCACTTTTACAGCATCAAGCAGTCCACAGCAGTGTGAGCT--CCAGGCCACA 539  
Qy 1431 GAGCAGCCCAAGAGTGTGCTGGGGGATGACGGCCAGGCTCCCTGACCACTCTGCTG 1490



RESULT 6  
US-11-136-527-2890  
; Sequence 2890, Application US/11136527  
; Publication No. US20050287570A1  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: Mounts, William M  
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes  
; FILE REFERENCE: 031896-041000 (AM101086)  
; CURRENT APPLICATION NUMBER: US/11/136,527  
; CURRENT FILING DATE: 2005-05-25  
; PRIOR APPLICATION NUMBER: US 60/574,294  
; PRIOR FILING DATE: 2005-05-26  
; NUMBER OF SEQ ID NOS: 362830  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 2890  
; LENGTH: 1815  
; TYPE: DNA  
; ORGANISM: Rattus norvegicus  
US-11-136-527-2890

Query Match 9.2%; Score 144.8; DB 12; Length 1815;  
Best Local Similarity 52.6%; Pred. No. 1.1e-26;  
Matches 426; Conservative 1; Mismatches 353; Indels 30; Gaps 4;

QY 602 GGAGCATCCGGTGCCTGCGAACAATCATCCACTGGAACTCATCTCGCCTTCATCTCTGC 661  
DB 715 GGAGGTGCACTGCACCTCGCACTACATCCACATGACACCTGTTCGTCTTCATCTCTGC 774  
QY 662 GCAACGCCACTGGTGTGGTGCAGTAACATAGAGCCCGAGGTCCACAGCAAC- 720  
DB 775 GCGCCCTGTCCAACTTCAATCAAGAGCCGCTACTCTTCTCTCGGACGAGTCACTACT 834  
QY 721 -----GTGGGCTGTGTGAGTGTGTGACAGCCGCTCAACTACTTCCATGTGA 769  
DB 835 GTGATGCCCAATAGTGGGTGCAAGCTGTGTGATGATCTTCTTCAGTACTGATCATG 894  
QY 770 CCAACTTCTTCTGGATGTTCGGGAGGGCTGTACTCTGCACACAGCCATCGTGTCTCACCT 829  
DB 895 CCAACTACGCATGGCTGTGTGGAGGGCTGTACTCTTCAACACTTCTTGGCCATCTCCT 954  
QY 830 ACTTCACTGACCGCTGCGCAATAGATGTTCATCTGCAATGGTGGGTGGTGGCTTCC 889  
DB 955 TCTTCTCAGAAAGAAAGTACTCTGAGGCCCTTGTGTCTCTCGATGGGTTCCTCAGCCA 1014  
QY 890 CCATCATTTGGCTGGCCATTTGGGAAGCTGTACTACGACATGAGAAAGTGTGTTG 949  
DB 1015 TTTTGTGTGTGTGGGCTATCACCAGGCATTTCTAGAAATATCTGGATGCTGG--G 1071  
QY 950 GCAAAAGGCTGGGGTGTACACGACTACATCTACAGGGCCCATGATCTGTCTCTGC 1009  
DB 1072 ACATCAAGCCATGTTCTCGTGTGGGTCACTCGAGGGCTGTGATCTGTCTCATTC 1131  
QY 1010 TGATCAATTTCACTTCTTTTCAACATCGTCGCAATCTCTATGACCAAGCTCCGGGCAT 1069  
DB 1132 TGATCAATTTCACTTCTTATAAACATCTTAAGAACTCTGATGAGGAAATCTAGAACAC 1191  
QY 1070 CCACCAAGTC-----TGAGACCAATTCAGTACAGGAAGGTGTGAAGCCACTCTGTGC 1123  
DB 1192 AAGAAACAAGAGAAAGTGAACAAACCAATTAAGCGCCTTGGCCAAAGTCCACCTCTCTGC 1251  
QY 1124 TGTGCGCCCTCTGGGCATCACTTACATGTCTTCTTGTCTTGTCTTGTCTTGTCTTGTCT 1183  
DB 1252 TGATCCGCTCTTTGGATCACTACATTTCTTGTCTTGTCTTGTCTTGTCTTGTCTTGTCT 1302  
QY 1184 TCTCCGGGTGCTTTCATCTTCACTTCAACTCTTCTTGTGGAATCTTCCAGGGCTTCTTTG 1243  
DB 1303 ACGCCATGAGGTCCAGCTGTCTTCTGAACTGGCCCTGGCTCTCTTCCAGGGTCTGTGTG 1362  
QY 1244 TGTCTGTGTCTTACTGTCTTCAATAGTAGGTCTGCTTCTGCAATCCGGAAGGTGGC 1303  
DB 1363 TAGCTGTCTTTTACTGTCTTCTCAATGTGAGGTGCAAGTTGGAAGTTTCAGAAAAATGGC 1422

QY 1304 ACCGGTGGCAGGACAAGCACTCGATCCGTGCCGAGTGGCCCTGCGCATGTCATCTCCCA 1363  
DB 1423 GCCAGTGGCACCCTTCAAGAGTTCCCGCTGCGCCTGTGGCCTTCAATAACTCTCTGACGA 1482  
QY 1364 CTTCCCAACCCCGTGTGTCAGCTTTCACAGCA 1393  
DB 1483 AGCCACCAACGCGCCCAACCCACAGCACCA 1512

RESULT 7  
US-11-136-527-2085  
; Sequence 2085, Application US/11136527  
; Publication No. US20050287570A1  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: Mounts, William M  
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes  
; FILE REFERENCE: 031896-041000 (AM101086)  
; CURRENT APPLICATION NUMBER: US/11/136,527  
; CURRENT FILING DATE: 2005-05-25  
; PRIOR APPLICATION NUMBER: US 60/574,294  
; PRIOR FILING DATE: 2005-05-26  
; NUMBER OF SEQ ID NOS: 362830  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 2085  
; LENGTH: 5192  
; TYPE: DNA  
; ORGANISM: Rattus norvegicus  
US-11-136-527-2085

Query Match 8.5%; Score 134.2; DB 12; Length 5192;  
Best Local Similarity 54.2%; Pred. No. 6.3e-24;  
Matches 396; Conservative 0; Mismatches 308; Indels 27; Gaps 5;

QY 601 AGGAGCATCCGGTGCCTGCGAACAATCATCCACTGGAACTCATCTCGCCTTCATCTCTG 660  
DB 2626 AGGAAGCTGCACTGTATCCCGAAACTATCATCCATGATCATCTTTCATGTCTTTCATCTCTG 2685  
QY 661 CGCAAGCCCACTGGTTC-----GTGGTCCAGCTAACCATGAGCCCGAGGTCCACCCAG 714  
DB 2686 AGGGCACTGCGCTCTTCATCAAGGACATGGCCCTCTTCAACAGCGGGAGATAGACCAC 2745  
QY 715 AGCAAGCTGGGT-----GGTGCAGGTGGTGACAGCGCCCTACAACTACTTCCATGTG 768  
DB 2746 TGCTCTGAGCCCTCGGTGGGTGCAAGGAGCGGTGTTTCTTCCAGTATTTGTGTCTG 2805  
QY 769 ACCAACTTCTTGTGATGTTCGGGAGGGCTGTACTGACACAGCCATCGTGTCTCACC 828  
DB 2806 GCCAACTTCTTGTGCTGTGTGAGGGCTTACTATACACCCCTGTCTGGCGGTCTCC 2865  
QY 829 TACTCCACTGACCGCTGCGCAATGGATGTTTCATCTGCAATTTGGTGGGTGTGCCCTTC 888  
DB 2866 TTCTTCTCGAGCGGAAGTACTTCTGCGGTACATTTCTCATCGCTGGGAGTGGCCAGT 2925  
QY 889 CCATCAATTTGGCCCTGGGCATTTGGGAAGCTGTACTACGCAATGAGAAAGTGTGTGTTT 948  
DB 2926 GTGTTTCATCAACCATATGACGCGTGTGAGGATATATTTGAGGATTTTCGGGTGTCTG 2982  
QY 949 GCGAAAGCGCTGGGTGTACCGGACTATCTACCGGGCCCATGATCTCTGTGTTCTG 1008  
DB 2983 GACACCATCATCAACTCTCTCTGTGTGGATCATAAAGGCCCCCATCTCTCTCTCCATC 3042  
QY 1009 CTGATCAATTTTCATCTTCTTTCATCATCGGATCTCTCATGACCAAGCTCCCGGCA 1068  
DB 3043 CTGTGAACTTCTGCTCTGTTTATCTGATCATCGGATCTCTGTTTCAAGAACTACGGCCA 3102  
QY 1069 TCCACC-----ACGCTGAGACCATTCAGTACAGGAAGCTGTGAAGCCACTTGTGGT 1122  
DB 3103 CCGGACATTTGGGAAGATGATAGCAGCCCATATTCGAGGTGCGCAAGTCCACGCTTCTG 3162  
QY 1123 CTGCTGCGCTCTCGGCATCACTACATGCTGTTCTTCTGCTCAATCCCGGGGAGGATGAG 1182

Db 3163 CTCATCCCTGTTGGAAATTCATATGTTGCTTCTTCCCGCAAACTCAAG 3222  
Qy 1183 GTCTCCGGGTGCTTCACTACTTCACTCTTCTTCTGGAATCCTTCCAGGCTCTTT 1242  
Db 3223 GCCAG-----GTGAAATGGTCTTGAATCTTGTGTGGGCTCTTTCAGGGTTCGTG 3276  
Qy 1243 GTGTCTGTGTCTACTGTTTCTCAATAGTAGAGTCCGTTCTGCCATCCCGGAAGAGGTGG 1302  
Db 3277 GTGGCCATCTCTACTGCTTCTCAATGTTGAGGTGACGGGAGCTGCGCGGAAGTGG 3336  
Qy 1303 CACCGGTGGCA 1313  
Db 3337 CGCGTTGGCA 3347

## RESULT 8

US-11-136-527-3765  
; Sequence 3765, Application US/11136527  
; Publication No. US20050287570A1  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: Mounts, William M  
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes  
; FILE REFERENCE: 031896-041000 (AM101086)  
; CURRENT APPLICATION NUMBER: US/11/136,527  
; CURRENT FILING DATE: 2005-05-25  
; PRIOR APPLICATION NUMBER: US 60/574,294  
; PRIOR FILING DATE: 2005-05-26  
; NUMBER OF SEQ ID NOS: 362830  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 3765  
; LENGTH: 3066  
; TYPE: DNA  
; ORGANISM: Rattus norvegicus  
US-11-136-527-3765

Query Match 8.2%; Score 129.6; DB 12; Length 3066;  
Best Local Similarity 52.0%; Pred. No. 8.2e-23;  
Matches 344; Conservative 0; Mismatches 309; Indels 9; Gaps 2;  
Qy 728 GGTGCAAGTTGGTGACAGCGCTTACAACTTCTCCATGTGACAACTTCTTCTGATGT 787  
Db 690 GCTGCGGACTGTGTCTCTCTCATGCAATCTGCGTGGCGGCAACTACTACTGTTGC 749  
Qy 788 TCGCGAGGCTGCTACTCTGACAGCCATCTGCTCACTACTCACTGACGGCTGC 847  
Db 750 TGTGGAAGCGGTATCTGTACACACTGTGCTGCTTCTCGGTGTTCTCGGACGCGCA 809  
Qy 848 GCAATGGATGTTTCATCTGCAATGGCTGGGCTGTGCCCTTCCCATCATTTGTGGCTGGG 907  
Db 810 TCTTCAAGCTGTACTGAGCATAGGCTGGGAGTTCGGCTGTCTGTTATCCCTGGG 869  
Qy 908 CAAATGGGAAGCTGTACTAGCAAAATGAGAAGTGTGTTTGGGAAAGCCCTGGGGTGT 967  
Db 870 GCATGTGTCAAGTATCTTACGAGGACGAGGGTGTCTG---ACCAGGAATCCCAACATGA 926  
Qy 968 ACACCGACTACATCTACAGGGGCGCATGATCTGCTGCTGCTGATCAATTTCTCTCC 1027  
Db 927 ACTATTGGCTCATCATACGTTGCCATCTCTTTTGAATCGGGGTCAACTTCTTGTCT 986  
Qy 1028 TTTTCAACATCGTCGGCATCTCATGACCAAGCTCCGGGATCCACCATCTGTGAGACCA 1087  
Db 987 TCATCCGGGTCACTGATCTGTATAGCAAGCTGAAGGCTATCTCATGTGTAGACCG 1046  
Qy 1088 TTCAGTACAGGAAGGTGTGAAGCCACTGTGTGTGCTGTGCTGCTGCTGCTGCTGCTTCA 1147  
Db 1047 ACATCAATACAGACTGCGGAAGTCCACTCTGACGCTCATCCGCTTCTGGGACGCGATG 1106  
Qy 1148 ACATGCTGTTCTTCTGCAATCCCGGGGAGGA-----TGAGGTCTCCGGGTGCTTCA 1201  
Db 1107 AAGTCATCTTTGCTTGTGATGAGCAGACGCCCGAGGAACCTTACGCTTCTGCTAAGC 1166  
Qy 1202 TCTACTTCAACTCTTCTGGAATCTCTTCCAGGGCTTCTTTGTGTCTGTTCTACTGTT 1261

Db 1167 TGTTCACAGAGCTCTCTTCACTTCTTCTTCCAGGGCTTATGTGGCTGTCTGTACTGCT 1226  
Qy 1262 TCTCTAATAGTAGGTCCGTTCTTCCATCCGGAAGAGGTGGCACCGGTGGCAGGACAAGC 1321  
Db 1227 TTTTCAACAATGAGTCCAGATGGAGTTTTCGGAAGAGCTGGGAGCGCTGGAGCTGGAGC 1286  
Qy 1322 ACTCGATCCGTCCCGAGTGGCGGTCATGTCCATCCCACTCCCAACCCCGGTGTC 1381  
Db 1287 GCTTGAACATCCAGAGGACAGCAGCATGAACCCCTCAAGTGTCTCCACAGCAGGTCA 1346  
Qy 1382 GC 1383  
Db 1347 GC 1348

## RESULT 9

US-11-136-527-1893  
; Sequence 1893, Application US/11136527  
; Publication No. US20050287570A1  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: Mounts, William M  
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes  
; FILE REFERENCE: 031896-041000 (AM101086)  
; CURRENT APPLICATION NUMBER: US/11/136,527  
; CURRENT FILING DATE: 2005-05-25  
; PRIOR APPLICATION NUMBER: US 60/574,294  
; PRIOR FILING DATE: 2005-05-26  
; NUMBER OF SEQ ID NOS: 362830  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 1893  
; LENGTH: 3453  
; TYPE: DNA  
; ORGANISM: Rattus norvegicus  
US-11-136-527-1893

Query Match 8.1%; Score 128.4; DB 12; Length 3453;  
Best Local Similarity 52.8%; Pred. No. 1.7e-22;  
Matches 323; Conservative 2; Mismatches 278; Indels 9; Gaps 2;  
Qy 709 CACGAGCAACGTGGGCTGTGTCAGGTTGGTGACAGCGCGCTTACAACTACTTCCATGTG 768  
Db 988 CATGACAGTGAAGTGAATGCAAGTTTGCAGATTTCTGCATTTTCCATCAGTACATGATGGCT 1047  
Qy 769 ACCAATCTTCTGATGTTCGGCAGGCTGTGCTACCTGCACACAGCCATCTGTCTCACC 828  
Db 1048 TGCACACTTCTGATGCTGTGTGAGGGGATCTATCTTCACTCTGATCGTATGGCT 1107  
Qy 829 TACTCCACTGACCGCTGGCAATGGAATGATGTTTCATCTGCAATGGCTGGGCTGTGCCCTTC 888  
Db 1108 GTGTTCAAGGATCAAGCTGTGCTGCTGCTATTTACTTTGGCTGGGGTTCCCAATA 1167  
Qy 889 CCCATCAATGTGGCTGGGCCATTTGGGAAGCTGTACTACGACAAATGAGAAGTGTCTGTTT 948  
Db 1168 GTGCCAACTATTATCCATGCCATTTACTGTGCGCTTATVTAACAAGCAACTGTTGGCT- 1226  
Qy 949 GGCAGAAAGCCCTGGGCTGTACACCGACTACCTACCGGGGCCCATGATCTGTGCTCTG 1008  
Db 1227 -----GAGTACGAGACCCCACTTGTCTTACATCATCCATGAGACCCCGTCTATGGCGGCTCTG 1281  
Qy 1009 CTGATCAATTTTCATCTTCTTTCATCGCTCGCATCTCATGACCAAGCTCCCGGCA 1068  
Db 1282 GTGGTCAATCTTCTTCTGCTCAACATTTGCTGGTGTCTTGTGACCAAGATGAGGCA 1341  
Qy 1069 TCCACCACTCTGAGACCAATTCAGTACAGGAAGGCTGTGAAGGCCCACTCTGTGTGCTG 1128  
Db 1342 ACCATGAAGCCGAGGCTTACATGTACCTGAAGGCTGTAAAGGCCCACTGTTGCTTGTG 1401  
Qy 1129 CCGCTCTGGGATCACTTACATGTCTGTTCTGCTCAATCCCGGGGAGGATGAGGTCTCC 1188  
Db 1402 CCGCTGCTGGGATCAGTTGTTGTTGTTTCCCTGGAGCCCTCCCAACAAAGTCT---T 1458

QY 1189 CGGGTGGTCTTCTATCTACTTCAACTCTTCTCGAATCCTTCCAGGCTCTTTGTGTCT 1248  
Db 1459 GGAAGATCTATGATATTATCTCATGCACTCTCTGATTCATTTCCAGGATCTTTGTGCG 1518  
QY 1249 GTGTCTACTGTTTCTCTCAATAGTAGGTCGGTTCTGCCATCCGAAGAGGTGGCACCGG 1308  
Db 1519 ACTATCTACTGTTCTCTTAACCATGAGTGAAGTGACCTCGAAGCGTCAAGTGGCGCAG 1578

QY 1309 TGGCAGGACAAAG 1320

Db 1579 TTCAAGATCCAG 1590

## RESULT 10

US-11-136-527-1894  
; Sequence 1894, Application US/11136527  
; Publication No. US20050287570A1  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: Mounts, William M  
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes  
; FILE REFERENCE: 031896-041000 (AMI101086)  
; CURRENT APPLICATION NUMBER: US/11/136,527  
; CURRENT FILING DATE: 2005-05-25  
; PRIOR APPLICATION NUMBER: US 60/574,294  
; PRIOR FILING DATE: 2005-05-26  
; NUMBER OF SEQ ID NOS: 362830  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 1894  
; LENGTH: 3434  
; TYPE: DNA  
; ORGANISM: Rattus norvegicus  
US-11-136-527-1894

Query/Match 7.9%; Score 124.6; DB 12; Length 3434;

Best Local Similarity 53.1%; Pred. No. 1.5e-21; Indels 9; Gaps 2;  
Matches 315; Conservative 0; Mismatches 269; Indels 9; Gaps 2;

QY 728 GGTGAGGTTGGTGACAGCGCCCTACAACTACTTCCATGTGACCACTTCTTCTGGATGT 787  
Db 949 GTTGCAAGATTCGTGCACTTTTTCATCAGTACATGATGGCTTGCACTACTTCTGGATGC 1008  
QY 788 TCGCGAGGGCTGCTACCTGACACAGCCATGTGTCACCTACTCAGTACGCGGTGC 847  
Db 1009 TGTGTGAGGGGATCTATCTTACACTCTGATCGTCATGGCTGTGTTCCACGAGGATCAAC 1068  
QY 848 GCAAAATGATGTTTCATCTGCACTGGCTGGGGTGTGCCCTTCCCATCATTTGTGCGCTGG 907  
Db 1069 GTCTGCGCTGGTACTATTATCTTGGCTGGGGGTTCCCATAGTGCCAACTATTATCCATG 1128  
QY 908 CCATTGGGAAGCTGTACTACGACAAATGAGAAGTGTGCTGTTTGGCAAAAGGCTGGGGTGT 967  
Db 1129 CCATTACTCGTGGCTACTACACGACAACTGTGGCTGAGTA-----CGGAGACCC 1182  
QY 968 ACACGACTACATCTACCGAGGCCCCATGATCTGTGCTGTGATCAATTTCACTTCC 1027  
Db 1183 ACTTGTCTTACATCATCCATGACCCCGTCTATGCGGGCTCTGGTGGTCAACTTCTTCTTTC 1242  
QY 1028 TTTTCAACATCGTCCGATCCTCATGACCAAGCTCCGGGATCCACACGTCTGAGACCA 1087  
Db 1243 TGCTCAACATGTGCGGTGCTGTGACCAAGATGAGGCAAAACCATGAGCCGAGGCT 1302  
QY 1088 TTCAGTACAGAAAGGCTGTGAAGACCACTCTGTGCTGTGCTGCCCTCTGGGATCACCT 1147  
Db 1303 ACATGTACCTGAAGGCTGTAAAGCCACCATGTCCTTGTGCCCCCTGCTGGGATCCAGT 1362  
QY 1148 ACATGCTGTTCTTGTCAATCCCGGGAGGATGAGGTCTCCCGGGTGTCTTCACTTACT 1207  
Db 1363 TTGTGTGTTTCCCTGGAGGCCCTCCCAACAAAGTGTCT---TGGGAAGATCTATGATTATC 1419  
QY 1208 TGAACCTCTTCTGGATCTCTTCAGGGCTCTTTGTGCTGTGTTCTACTGTTCTCTCA 1267  
Db 1420 TCATGCACTCTCTGATTTTCAGGGATTTCTTTGTGCGGACTATCTACTGCTTCTGTA 1479

QY 1268 ATAGTGAAGTCCGTTCTGCCATCCGAAGAGGTGGCAACCGGTGGCAGGACAAG 1320  
Db 1480 ACCATGAGGTGCAAGTGAACCTGAAGCGTCAGTGGCGGAGTTCAAGATCCAG 1532

## RESULT 11

US-09-925-065A-506766/c  
; Sequence 506766, Application US/09925065A  
; Publication No. US20040181048A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single  
; FILE REFERENCE: Nucleotide Polymorphisms in the Human Genome  
; CURRENT APPLICATION NUMBER: US/09/925,065A  
; CURRENT FILING DATE: 2001-08-08  
; PRIOR APPLICATION NUMBER: US 60/243,096  
; PRIOR FILING DATE: 2000-10-24  
; PRIOR APPLICATION NUMBER: US 60/252,147  
; PRIOR FILING DATE: 2000-11-20  
; PRIOR APPLICATION NUMBER: US 60/250,092  
; PRIOR FILING DATE: 2000-11-30  
; PRIOR APPLICATION NUMBER: US 60/261,766  
; PRIOR FILING DATE: 2001-01-16  
; PRIOR APPLICATION NUMBER: US 60/289,846  
; PRIOR FILING DATE: 2001-05-09  
; NUMBER OF SEQ ID NOS: 957086  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 506766  
; LENGTH: 613  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-925-065A-506766

Query/Match 7.8%; Score 124; DB 6; Length 613;

Best Local Similarity 100.0%; Pred. No. 1.5e-21; Indels 0; Gaps 0;  
Matches 124; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 601 AGGAGCATCCGGTGCCTGGAAACATCATCCACTGGAACCTCATCTCCGCTTTCATCCTG 660  
Db 356 AGGAGCATCCGGTGCCTGGAAACATCATCCACTGGAACCTCATCTCCGCTTTCATCCTG 297  
QY 661 CGCAACGCCACCTGTGTCGTGTCAGCTAACCATGAGCCCGAGGTCCACCAAGAGCAAC 720  
Db 296 CGCAACGCCACCTGTGTCGTGTCAGCTAACCATGAGCCCGAGGTCCACCAAGAGCAAC 237  
QY 721 GTGG 724  
Db 236 GTGG 233

## RESULT 12

US-11-136-527-4065  
; Sequence 4065, Application US/11136527  
; Publication No. US20050287570A1  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: Mounts, William M  
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes  
; FILE REFERENCE: 031896-041000 (AMI101086)  
; CURRENT APPLICATION NUMBER: US/11/136,527  
; CURRENT FILING DATE: 2005-05-25  
; PRIOR APPLICATION NUMBER: US 60/574,294  
; PRIOR FILING DATE: 2005-05-26  
; NUMBER OF SEQ ID NOS: 362830  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 4065  
; LENGTH: 1806  
; TYPE: DNA  
; ORGANISM: Rattus norvegicus  
US-11-136-527-4065





[illegible]

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; FILE REFERENCE: 01997.027700
; CURRENT APPLICATION NUMBER: US/11/128,049
; CURRENT FILING DATE: 2005-05-11
; PRIOR APPLICATION NUMBER: US 60/570,425
; PRIOR FILING DATE: 2004-05-11
; NUMBER OF SEQ ID NOS: 7285
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 870
; LENGTH: 2786
; TYPE: DNA
; ORGANISM: Cricetulus sp.
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (132)..(151)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1560)..(1607)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (2217)..(2276)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (2561)..(2580)
; OTHER INFORMATION: n is a, c, g, or t
; US-11-128-049-870

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RESULT 15
US-11-128-049-870
; Sequence 870, Application US/11128049
; Publication No. US20060010513A1
; GENERAL INFORMATION:
; APPLICANT: Melville, Mark W.
; APPLICANT: Charlebois, Timothy S.
; APPLICANT: Mounts, William M.
; APPLICANT: Hann, Louane E.
; APPLICANT: Sinacore, Martin S.
; APPLICANT: Leonard, Mark W.
; APPLICANT: Brown, Eugene L.
; APPLICANT: Miller, Christopher P.
; TITLE OF INVENTION: OLIGONUCLEOTIDE ARRAYS
; TITLE OF INVENTION: MAKING AND USING SAME
FOR

```

Search completed: March 17, 2006, 11:08:49  
Job time : 583 secs

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GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: March 16, 2006, 17:12:55 ; Search time 192 Seconds  
(without alignments)  
1016.063 Million cell updates/sec

Title: US-10-649-193-15  
Perfect score: 2381  
Sequence: 1 MGHQPQLRVKALLLGLNP.....SIPTSPTRVSFHSIKOSTAV 444

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_21.\*

- 1: Geneseqp1980s.\*
- 2: Geneseqp1990s.\*
- 3: Geneseqp2000s.\*
- 4: Geneseqp2001s.\*
- 5: Geneseqp2002s.\*
- 6: Geneseqp2003as.\*
- 7: Geneseqp2003bs.\*
- 8: Geneseqp2004s.\*
- 9: Geneseqp2005s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2381	100.0	444	4	AAB71866 Human CRF
2	2381	100.0	444	5	AAB71866 Human CRF
3	2381	100.0	444	6	AAB71866 Human CRF
4	2381	100.0	444	6	ABU08081 Human cor
5	2381	100.0	444	6	ABG76402 Human hCR
6	2381	100.0	444	7	ADJ65810 Human Pro
7	2381	100.0	444	8	ADJ65810 Human cor
8	2324	97.6	447	7	ADJ65810 Human cor
9	2186.5	91.8	415	2	AAR69519 Human pit
10	2186.5	91.8	415	2	AAR69519 Human cor
11	2186.5	91.8	415	2	AAR69519 Human cor
12	2186.5	91.8	415	5	AAR69519 Human cor
13	2186.5	91.8	415	5	AAO19420 Human cor
14	2186.5	91.8	415	5	AAO19421 Human cor
15	2186.5	91.8	415	5	ABG66957 Human cor
16	2186.5	91.8	415	5	ABR43051 Human cor
17	2186.5	91.8	415	6	ABU08075 Human cor
18	2186.5	91.8	415	6	ABG76046 Human cor
19	2186.5	91.8	415	8	ADJ65797 Human cor
20	2186.5	91.8	415	8	ADO29265 Human GPC
21	2186.5	91.8	415	8	ADO50785 Human cor
22	2186.5	91.8	415	8	ADO50783 Human cor
23	2180.5	91.6	415	4	ABBS6345 Non-endog
24	2137.5	89.8	415	2	AAR97294 Mouse CRF

25	2137.5	89.8	415	5	AAE26684	Aae26684 Mouse CRF
26	2137.5	89.8	415	5	AAO19430	Aao19430 Murine co
27	2137.5	89.8	415	6	ABR43059	Abr43059 Mouse CRH
28	2137.5	89.8	415	6	ABU08080	Abu08080 Mouse cor
29	2137.5	89.8	415	6	ABG76401	Abg76401 Mouse cor
30	2137.5	89.8	415	8	ADJ65808	Adj65808 Mouse cor
31	2137.5	89.8	415	8	ADO29266	Ado29266 Mouse GPC
32	2137.5	89.8	415	8	ADO50803	Ado50803 mouse cor
33	2126.5	89.3	415	2	AAR69521	Aar69521 Rat corti
34	2126.5	89.3	415	2	AAR97292	Aar97292 Rat CRF r
35	2126.5	89.3	415	2	ABU62361	Abu62361 Rat corti
36	2126.5	89.3	415	5	AAE26681	Aae26681 Rat CRF-R
37	2126.5	89.3	415	5	AAO19427	Aao19427 Rat corti
38	2126.5	89.3	415	5	AAO19439	Aao19439 Bovine co
39	2126.5	89.3	415	6	ABU08077	Abu08077 Rat corti
40	2126.5	89.3	415	6	ABG76048	Abg76048 Rat Prote
41	2126.5	89.3	415	7	ADJ65801	Adj65801 Rat corti
42	2126.5	89.3	415	8	ADJ65801	Adj65801 Rat corti
43	2126.5	89.3	415	8	ADO50797	Ado50797 Rat corti
44	2126.5	89.3	415	8	ADO50821	Ado50821 Cow corti
45	2092.5	87.9	401	5	AAU96998	Aau96998 Human CRH

ALIGNMENTS

RESULT 1  
AAB71866

ID AAB71866 standard; protein; 444 AA.

XX AAB71866;

XX 03-MAY-2001 (first entry)

XX Human CRF1 seven transmembrane domain.

XX Human; CRF1; corticotropin releasing factor receptor 1; h15571;  
XX immunomodulatory; vascular; hepatic; antiasthma; antimicrobial;  
XX antiinflammatory; immunosuppressive; gene therapy; vaccine;  
XX G-protein coupled receptor; GPCR; liver fibrosis; respiratory disorder;  
XX infection; chronic inflammatory disease; organ-specific autoimmunity;  
XX graft rejection; cystic fibrosis.

XX Homo sapiens.

XX WO200109328-A1.

XX 08-FEB-2001.

XX 03-AUG-2000; 2000WO-US021278.

XX 03-AUG-1999; 99US-0146916P.

XX 29-FEB-2000; 2000US-00515781.

XX (MILL-) MILLENNIUM PHARM INC.

XX Hodge MR, Lloyd C, Welch NS;

XX WPI; 2001-138653/14.

XX Nucleic acids encoding a G-prot. coupled receptor polypeptides, useful  
XX for preventing, diagnosing and treating, e.g. liver fibrosis and asthma.  
XX Disclosure; Fig 2; 145pp; English.

XX The present sequence is a human G-protein coupled receptor (GPCR) used  
XX for comparison with the seven transmembrane domain of a novel GPCR  
XX designated h15571. h15571 GPCR polynucleotides and polypeptides may be  
XX used in the prevention, treatment and diagnosis of diseases associated  
XX with inappropriate GPCR expression. Such diseases include immune,  
XX haematological, fibrotic, hepatic and respiratory disorders including  
XX asthma, allergies (e.g. allergic rhinitis and psoriasis), pathogenic  
XX infections, chronic inflammatory diseases, organ-specific autoimmunity,

CC graft rejection, graft versus host disease, cystic fibrosis and, in  
 CC particular, liver fibrosis. The GPCR polypeptides may be used as antigens  
 CC in the production of antibodies against GPCR and in assays to identify  
 CC modulators (agonists and antagonists) of GPCR expression and activity.  
 CC The anti-GPCR antibodies and GPCR antagonists may also be used to down  
 CC regulate GPCR expression and activity. The anti-GPCR antibodies may be  
 CC used as diagnostic agents for detecting the presence of GPCR polypeptides  
 CC in samples  
 XX  
 SQ Sequence 444 AA;

Query Match 100.0%; Score 2381; DB 4; Length 444;  
 Best Local Similarity 100.0%; Pred. No. 8.9e-245;  
 Matches 444; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MGGHPQLRLVKALLLLGLNPNVSASLQDHCESLSLASNISGLQCNASVDLIGTCWPRSPA 60  
 DB 1 MGGHPQLRLVKALLLLGLNPNVSASLQDHCESLSLASNISGLQCNASVDLIGTCWPRSPA 60  
 QY 61 GOLVVRPCPAFFYGVRYNTTNGYRECLANGSWAARVNYSECQIILNEEKSKVHVHVAV 120  
 DB 61 GOLVVRPCPAFFYGVRYNTTNGYRECLANGSWAARVNYSECQIILNEEKSKVHVHVAV 120  
 QY 121 IINYLGHCSILVALLVAFVFLRLRPGCTHWGDAQDGALEVGAPWPGAPFQVRSIRCLR 180  
 DB 121 IINYLGHCSILVALLVAFVFLRLRPGCTHWGDAQDGALEVGAPWPGAPFQVRSIRCLR 180  
 QY 181 NIIHWNLSAFILRNATWVQLTMSPEVHQSNVGCRLVTAAYNYFHTNPFWMFGECC 240  
 DB 181 NIIHWNLSAFILRNATWVQLTMSPEVHQSNVGCRLVTAAYNYFHTNPFWMFGECC 240  
 QY 241 YLHTAIVLTYSTDLRKKMFCIGMGVPPFIIVAWAIGKLYDNEKCFKRGKRGVVTDIY 300  
 DB 241 YLHTAIVLTYSTDLRKKMFCIGMGVPPFIIVAWAIGKLYDNEKCFKRGKRGVVTDIY 300  
 QY 301 YQGPMLVLLINFIPLFNIVRLMTKLRASTTSETIQYRKAVKATLVLLPLLGITYMLFF 360  
 DB 301 YQGPMLVLLINFIPLFNIVRLMTKLRASTTSETIQYRKAVKATLVLLPLLGITYMLFF 360  
 QY 361 VNPGEDEVSRVVIYFNFSFLESFQGFVSVFYCFLNSEVRSAIRKRWHRQDKHSIRARV 420  
 DB 361 VNPGEDEVSRVVIYFNFSFLESFQGFVSVFYCFLNSEVRSAIRKRWHRQDKHSIRARV 420  
 QY 421 ARAMSIPTSPTRVSPHSIKOSTAV 444  
 DB 421 ARAMSIPTSPTRVSPHSIKOSTAV 444

RESULT 2  
 AAE26685  
 ID AAE26685 standard; protein; 444 AA.  
 XX  
 AC AAE26685;  
 XX  
 DT 13-DEC-2002 (first entry)  
 DE Human CRF-RA2 splice variant protein.  
 XX  
 KW Human; G protein-coupled corticotropin-releasing factor receptor; CRF;  
 KW CRF-R; adrenocorticotrophic hormone; irritable bowel syndrome; therapy;  
 KW Cushing's syndrome; pituitary tumour; chronic stress; anorexia nervosa;  
 KW receptor; alcoholism; CRF-RA2.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US2002055617-A1.  
 XX  
 PD 09-MAY-2002.  
 XX  
 PF 12-NOV-1998; 98US-00191724.  
 XX  
 PR 18-JUN-1993; 93US-00079320.  
 PR 23-AUG-1993; 93US-00110286.

PR 25-MAY-1994; 94WO-US005908.  
 PR 09-DEC-1994; 94US-00353537.  
 PR 07-JUN-1995; 95US-00483139.  
 XX  
 PA (PERR/) PERRIN M H.  
 PA (CHEN/) CHEN R.  
 PA (LEW/) LEWIS K A.  
 PA (VALE/) VALE W W.  
 PA (DONA/) DONALDSON C J.  
 PA (SAWC/) SAWCHENKO P.  
 XX  
 PI Perrin MH, Chen R, Lewis KA, Vale WM, Donaldson CJ, Sawchenko P;  
 XX  
 DR WPI: 2002-462916/49.  
 DR N-PSDB; AAD44489.  
 XX  
 PT New isolated recombinant mammalian G protein-coupled corticotropin-  
 PT releasing factor receptor protein for treating e.g. Cushing's syndrome,  
 PT pituitary tumors, stress, anorexia, alcoholism or irritable bowel  
 PT syndrome.  
 XX  
 PS Claim 9; Page 33-34; 44pp; English.  
 XX  
 CC The invention relates to recombinant mammalian G protein-coupled  
 CC corticotropin-releasing factor (CRF) receptor (CRF-R) proteins having  
 CC high affinity for CRF and nucleic acid molecules encoding such receptor  
 CC proteins. Polypeptides of the invention can be used to reduce high levels  
 CC of adrenocorticotrophic hormone caused by excess CRF and so can be used  
 CC to treat diseases such as Cushing's syndrome, pituitary tumours, chronic  
 CC stress, anorexia nervosa, alcoholism and irritable bowel syndrome. They  
 CC are used in pharmaceuticals and in the production of antibodies. The  
 CC present sequence is human CRF-RA2 splice variant protein  
 XX  
 SQ Sequence 444 AA;

Query Match 100.0%; Score 2381; DB 5; Length 444;  
 Best Local Similarity 100.0%; Pred. No. 8.9e-245;  
 Matches 444; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MGGHPQLRLVKALLLLGLNPNVSASLQDHCESLSLASNISGLQCNASVDLIGTCWPRSPA 60  
 DB 1 MGGHPQLRLVKALLLLGLNPNVSASLQDHCESLSLASNISGLQCNASVDLIGTCWPRSPA 60  
 QY 61 GOLVVRPCPAFFYGVRYNTTNGYRECLANGSWAARVNYSECQIILNEEKSKVHVHVAV 120  
 DB 61 GOLVVRPCPAFFYGVRYNTTNGYRECLANGSWAARVNYSECQIILNEEKSKVHVHVAV 120  
 QY 121 IINYLGHCSILVALLVAFVFLRLRPGCTHWGDAQDGALEVGAPWPGAPFQVRSIRCLR 180  
 DB 121 IINYLGHCSILVALLVAFVFLRLRPGCTHWGDAQDGALEVGAPWPGAPFQVRSIRCLR 180  
 QY 181 NIIHWNLSAFILRNATWVQLTMSPEVHQSNVGCRLVTAAYNYFHTNPFWMFGECC 240  
 DB 181 NIIHWNLSAFILRNATWVQLTMSPEVHQSNVGCRLVTAAYNYFHTNPFWMFGECC 240  
 QY 241 YLHTAIVLTYSTDLRKKMFCIGMGVPPFIIVAWAIGKLYDNEKCFKRGKRGVVTDIY 300  
 DB 241 YLHTAIVLTYSTDLRKKMFCIGMGVPPFIIVAWAIGKLYDNEKCFKRGKRGVVTDIY 300  
 QY 301 YQGPMLVLLINFIPLFNIVRLMTKLRASTTSETIQYRKAVKATLVLLPLLGITYMLFF 360  
 DB 301 YQGPMLVLLINFIPLFNIVRLMTKLRASTTSETIQYRKAVKATLVLLPLLGITYMLFF 360  
 QY 361 VNPGEDEVSRVVIYFNFSFLESFQGFVSVFYCFLNSEVRSAIRKRWHRQDKHSIRARV 420  
 DB 361 VNPGEDEVSRVVIYFNFSFLESFQGFVSVFYCFLNSEVRSAIRKRWHRQDKHSIRARV 420  
 QY 421 ARAMSIPTSPTRVSPHSIKOSTAV 444  
 DB 421 ARAMSIPTSPTRVSPHSIKOSTAV 444

RESULT 3

ABR43052  
 ID ABR43052 standard; protein; 444 AA.  
 XX  
 AC ABR43052;  
 XX  
 DT 03-JUL-2003 (first entry)  
 XX  
 DE Human CRH-R1 beta protein SEQ ID NO:2.  
 XX  
 KW Human; corticotropin releasing hormone receptor type 1; CRH-R1;  
 KW antipsoriatic; antiallergic; immunosuppressive; antiinflammatory;  
 KW dermatological; pathophysiological state; neuroendocrine disorder;  
 KW hyperproliferative epidermal disorder; allergic contact dermatitis;  
 KW autoimmune disorder; epidermal carcinogenesis; malignant transformation;  
 KW epidermal melanocyte; dermal melanocyte; chromosome 17.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2003024990-A2.  
 XX  
 PD 27-MAR-2003.  
 XX  
 PF 13-SEP-2002; 2002WO-US029117.  
 XX  
 PR 14-SEP-2001; 2001US-0322195P.  
 XX  
 PA (UYTE-) UNIV TENNESSEE RES CORP.  
 XX  
 PI Pisarchik A, Slominski A;  
 XX  
 DR WPI; 2003-313342/30.  
 XX  
 PT Novel DNA encoding corticotropin releasing hormone receptor type 1 which  
 PT is useful for treating pathophysiological state such as inflammatory skin  
 PT disease e.g. psoriasis and allergic contact dermatitis.  
 XX  
 PS Example 5; Fig 5A-C; 110pp; English.  
 XX  
 CC The present invention describes DNA (I) encoding a corticotropin  
 CC releasing hormone receptor type 1 (CRH-R1) protein comprising an amino  
 CC acid sequence given in ABR43055 to ABR43071. Also describe: (1) a vector  
 CC (II) capable of expressing (I) or its degenerate variant, and comprising  
 CC (1) or its degenerate variant, and regulatory elements necessary for  
 CC expression of the DNA in a cell; (2) a host cell (III) transfected with  
 CC (II); (3) an isolated CRH-R1 protein (IV) encoded by (I); (4) an antibody  
 CC (V) directed against (IV); (5) a pharmaceutical composition (VI)  
 CC comprising (IV), and a carrier; and (6) protecting (M) skin cells against  
 CC damage induced by an environmental factor, by inducing the expression of  
 CC CRH-R type Ig in the skin cells, where the expression of the receptor  
 CC protects the skin cells against the damage. CRH-R1 has antipsoriatic,  
 CC antiallergic, immunosuppressive, antiinflammatory and dermatological  
 CC activities. (VI) can be used for treating a pathophysiological state such  
 CC as hyperproliferative epidermal disorder, neuroendocrine disorder,  
 CC allergic contact dermatitis, autoimmune disorder, epidermal  
 CC carcinogenesis, malignant transformation of epidermal or dermal  
 CC melanocytes. (M) is useful for protecting (M) skin cells against damage  
 CC induced by an environmental factor such as solar radiation. Human CRH-R1  
 CC is located on chromosome 17, and mouse CRH-R1 is located to chromosome  
 CC 11. The present sequence represents human CRH-R1 beta (see Genbank  
 CC accession number U23333), which is used in the exemplification of the  
 CC present invention  
 XX  
 SQ Sequence 444 AA;  
 XX

Query Match 100.0%; Score 2381; DB 6; Length 444;  
 Best Local Similarity 100.0%; Pred. No. 8.9e-245;  
 Matches 444; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 XX

QY 1 MGGHPQLRLVKAALLGLNPNVSLQDQHCESLSLASNISGLQCNASVDLIGTCWPRSPA 60  
 DB 1 MGGHPQLRLVKAALLGLNPNVSLQDQHCESLSLASNISGLQCNASVDLIGTCWPRSPA 60  
 QY 61 GQLVVRPCPAFFYGVRYNTTNGYRECLANGSWAARNVYSECEILNEEKSKVHYHAV 120

Db 61 GQLVVRPCPAFFYGVRYNTTNGYRECLANGSWAARNVYSECEILNEEKSKVHYHAV 120  
 QY 121 IINYLGHICISLVALLVAFVLFLRLRPGCTHWGDAQDGALEVGAPWSGAPQVRSIRCLR 180  
 Db 121 IINYLGHICISLVALLVAFVLFLRLRPGCTHWGDAQDGALEVGAPWSGAPQVRSIRCLR 180  
 QY 181 NIIHWNLIISAFILRNATFWVQLTMSPEVHQSNVGCRLVTAAYNYFHVTFNPFWMGEGC 240  
 Db 181 NIIHWNLIISAFILRNATFWVQLTMSPEVHQSNVGCRLVTAAYNYFHVTFNPFWMGEGC 240  
 QY 241 YLHTALVLVYSTDLRKWMFICIGWGPVPIIIVAWAIGKLYYDNEKWCWFKRGKRGVYTDYI 300  
 Db 241 YLHTALVLVYSTDLRKWMFICIGWGPVPIIIVAWAIGKLYYDNEKWCWFKRGKRGVYTDYI 300  
 QY 301 YQGPMLVLLINFIPLFNIVRIILMTKLRASTTSETIOYRKAVKATILVLLPLLGITYMLFF 360  
 Db 301 YQGPMLVLLINFIPLFNIVRIILMTKLRASTTSETIOYRKAVKATILVLLPLLGITYMLFF 360  
 QY 361 VNPGEDEVSRVFIYFNSFLESFQGFVSFVFCFLNSEVRSAIRKRWHRWQDKHSIRARV 420  
 Db 361 VNPGEDEVSRVFIYFNSFLESFQGFVSFVFCFLNSEVRSAIRKRWHRWQDKHSIRARV 420  
 QY 421 ARAMSIPTSPTRVSPHSIKOSTAV 444  
 Db 421 ARAMSIPTSPTRVSPHSIKOSTAV 444

RESULT 4  
 ID ABR43052 standard; protein; 444 AA.  
 XX  
 AC ABR43052;  
 XX  
 DT 21-MAY-2003 (first entry)  
 XX  
 DE Human corticotropin-releasing factor receptor 2 (CRF-R2).  
 XX  
 KW Human; receptor; corticotropin-releasing factor receptor; CRF;  
 KW G protein-coupled corticotropin-releasing factor receptor;  
 KW hypothalamic peptide; pituitary adrenocorticotrophic hormone; ACTH;  
 KW adrenal glucocorticoid; gene therapy; cortisol; Alzheimer's disease;  
 KW Cushing's disease; anorexia nervosa; alcoholism; antiinflammatory;  
 KW irritable bowel syndrome; melancholic depression; neuroprotective;  
 KW nootropic; antidepressant; splice variant.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US6495343-B1.  
 XX  
 PD 17-DEC-2002.  
 XX  
 PF 17-JAN-1995; 95US-00374009.  
 XX  
 PR 18-JUN-1993; 93US-00079320.  
 PR 23-AUG-1993; 93US-00110286.  
 PR 25-MAY-1994; 94WO-US005908.  
 PR 09-DEC-1994; 94US-00353537.  
 XX  
 PA (SALK ) SALK INST BIOLOGICAL STUDIES.  
 XX  
 PI Ferrin MH, Chen R, Lewis KA, Vale WW, Donaldson CJ, Sawchenko P;  
 XX  
 DR WPI; 2003-327461/31.  
 XX  
 DR N-PSDB; ABX93041.  
 XX  
 PT New nucleic acid and its encoded G protein-coupled corticotropin-  
 PT releasing factor receptor, useful for diagnosing or treating e.g. ACTH  
 PT levels or high cortisol levels associated with Alzheimer's disease or  
 PT Cushing's disease.  
 XX  
 PS Disclosure; Col 61-64; 42pp; English.  
 XX

CC The invention discloses an isolated nucleic acid, which encodes a  
CC mammalian G protein-coupled corticotropin-releasing factor (CRF) receptor  
CC protein. CRF is a hypothalamic peptide which stimulates the secretion and  
CC biosynthesis of pituitary adrenocorticotrophic hormone (ACTH) leading to  
CC increased adrenal glucocorticoid production. The nucleic acid, or the CRF  
CC receptor that it encodes, is useful in bioassays. The nucleic acid or CRF  
CC receptor is particularly useful for providing recombinant receptors that  
CC allows the development of less expensive, more sensitive and automated  
CC means for assaying CRF and CRF-like compounds and developing CRF-based  
CC therapeutics. The nucleic acid, or fragments of its encoded receptor, are  
CC useful in therapy, e.g. gene therapy for reducing ACTH levels or treating  
CC high cortisol levels associated with Alzheimer's diseases, Cushing's  
CC diseases, anorexia nervosa, alcoholism or irritable bowel syndrome. These  
CC are also useful in diagnostic assays, e.g. for diagnosing Alzheimer's  
CC diseases, melancholic depression, anorexia nervosa, Cushing's diseases or  
CC alcoholism. The sequence presented is the human splice variant of CRF-R1,  
CC CRF-R2, protein  
XX  
XX  
SQ Sequence 444 AA;

Query Match 100.0%; Score 2381; DB 6; Length 444;  
Best Local Similarity 100.0%; Pred. No. 8.9e-245;  
Matches 444; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGGHPQLRLVKALLGLNPVSASLQDQCESLSLASNISGLQCNASVDLIGTCWPRSPA 60  
Db 1 MGGHPQLRLVKALLGLNPVSASLQDQCESLSLASNISGLQCNASVDLIGTCWPRSPA 60  
QY 61 GOLVVRPCPAFFYGVRYNTNNGYRECLANGSWAARVNYSECOEILNEEKSKVHYHVAV 120  
Db 61 GOLVVRPCPAFFYGVRYNTNNGYRECLANGSWAARVNYSECOEILNEEKSKVHYHVAV 120  
QY 121 IINYLGHCSLVALLVAFVLFLRLPQCTHWGDAQDALEVGAPWGSAPPQVRSIRCLR 180  
Db 121 IINYLGHCSLVALLVAFVLFLRLPQCTHWGDAQDALEVGAPWGSAPPQVRSIRCLR 180  
QY 181 NIIHWNLSAFILRNATFWVQLTMSPEVHQSNVGCRLVTAAYNFHVTFNFMFGEGC 240  
Db 181 NIIHWNLSAFILRNATFWVQLTMSPEVHQSNVGCRLVTAAYNFHVTFNFMFGEGC 240  
QY 241 YLHTAIVLYSTDRLRKWPFCIGWGVPPIIVAMAIGKLYDNEKWCWGRKPGVYTDYI 300  
Db 241 YLHTAIVLYSTDRLRKWPFCIGWGVPPIIVAMAIGKLYDNEKWCWGRKPGVYTDYI 300  
QY 301 YQGPMLVLLINFIPLFNVIILMTKLRASTTSETIQYKAVKATVLLPLLGITVWLFF 360  
Db 301 YQGPMLVLLINFIPLFNVIILMTKLRASTTSETIQYKAVKATVLLPLLGITVWLFF 360  
QY 361 VNPGEDEVSRVFIYFNSFLESFQGFVSVFYCFNLSEVRSAIRKRWHRWQDKHSIRARV 420  
Db 361 VNPGEDEVSRVFIYFNSFLESFQGFVSVFYCFNLSEVRSAIRKRWHRWQDKHSIRARV 420  
QY 421 ARAMSIPTSPTRVSHSIKQSTAV 444  
Db 421 ARAMSIPTSPTRVSHSIKQSTAV 444

RESULT 5  
ABG76402  
ID ABG76402 standard; protein; 444 AA.  
XX  
XX ABG76402;  
XX  
DT 07-MAY-2003 (first entry)  
XX  
DE Human hCRF-R1, splice variant.  
XX  
KW Human; receptor; corticotropin releasing factor receptor; hCRF-R1;  
KW Cushing's disease; pituitary tumour; Alzheimer's disease;  
KW melancholic depression; anorexia nervosa; chronic stress; alcoholism;  
KW hypercortisolemia; gastrointestinal disorder; irritable bowel syndrome;  
KW pre-eclampsia; pregnancy-induced complication; arthritis; abortion;  
KW twinning.

XX Homo sapiens.  
OS  
XX US6482608-B1.  
PN  
XX 19-NOV-2002.  
PD  
XX 26-MAY-2000; 2000US-00580734.  
PF  
XX 18-JUN-1993; 93US-00079320.  
PR 23-AUG-1993; 93US-00110286.  
PR 25-MAY-1994; 94WO-US0005908.  
PR 09-DEC-1994; 94WO-00353537.  
PR 17-JAN-1995; 95US-00374009.  
PR 07-JUN-1995; 95US-00483139.  
PR 12-NOV-1998; 98US-00191724.  
XX  
XX (SALK ) SALK INST BIOLOGICAL STUDIES.  
XX  
XX Perrin MH, Chen R, Lewis KA, Vale WW, Donaldson CJ, Sawchenko P;  
PI  
XX WPI: 2003-287359/28.  
XX N-PSDB; ABX11840.  
DR  
XX  
PT Novel cell line expressing nucleic acid expression vector comprising  
PT nucleic acid encoding human corticotropin releasing factor (CRF) receptor  
PT useful for reducing high adrenocorticotropin hormone, by binding to CRF.  
XX  
PS Disclosure; Col 61-64; 42pp; English.  
CC  
CC The invention relates to a cell line expressing a recombinant  
CC corticotropin releasing factor receptor (CRF-R) encoded by a nucleic acid  
CC expression vector, or a cell line containing a nucleic acid vector  
CC encoding a recombinant CRF-R. The vector encodes human CRF-R, subtype A,  
CC variant 1 (hCRF-R1). Also included is expressing a recombinant CRF  
CC receptor in a suitable host cell, by expressing the vector, where the  
CC nucleic acid encodes CRF-R that binds CRF or nucleic acid degenerate to  
CC the naturally occurring nucleic acid. The cell line is useful for  
CC expressing hCRF-R1 protein by recombinant techniques and in binding  
CC assays using CRF-R which are used for rapidly screening large number of  
CC compounds to determine which compounds are capable of binding to CRF-R,  
CC and for identifying new CRF-like ligands. The polypeptides expressed by  
CC the cell line inhibit CRF binding to CRF-R and can inhibit CRF-induced  
CC adrenocorticotropin hormone (ACTH) release in vitro by several cells, and  
CC so are useful for reducing high ACTH levels caused by excess CRF, and for  
CC treating Cushing's disease, pituitary tumours, Alzheimer's disease, and  
CC melancholic depression, anorexia nervosa, chronic stress, alcoholism and  
CC hypercortisolemia. The proteins are also useful for treating  
CC gastrointestinal disorders such as irritable bowel syndrome,  
CC abnormalities such as pre-eclampsia, which occur during pregnancy, to  
CC reduce pregnancy-induced complications and increased CRF levels which can  
CC otherwise result in excessive release of ACTH. The proteins are also  
CC useful for locally treating arthritis and other similar ailments,  
CC modulating action of CRF in mammals, treating the pregnancy-related  
CC pathological disorders in mammals. The CRF-R polypeptides are used in  
CC such areas as the diagnosis and/or treatment of CRF-dependent tumours,  
CC enhancing the survival of brain neurons, inducing abortion in livestock  
CC and other domesticated animals, inducing twinning in livestock and other  
CC domesticated animals. The present sequence represents a splice variant of  
CC human corticotropin releasing factor receptor, hCRF-R1  
XX  
XX Sequence 444 AA;  
SQ  
Query Match 100.0%; Score 2381; DB 6; Length 444;  
Best Local Similarity 100.0%; Pred. No. 8.9e-245;  
Matches 444; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MGGHPQLRLVKALLGLNPVSASLQDQCESLSLASNISGLQCNASVDLIGTCWPRSPA 60  
Db 1 MGGHPQLRLVKALLGLNPVSASLQDQCESLSLASNISGLQCNASVDLIGTCWPRSPA 60  
QY 61 GOLVVRPCPAFFYGVRYNTNNGYRECLANGSWAARVNYSECOEILNEEKSKVHYHVAV 120  
|||

Db 61 GQLVVRPCPAFFYGVRYNTTNGYRECLANGSWAARVNSECOEILNEEKSKVHHVAV 120  
QY 121 IINYLGHCSISLVALLVAFVFLFLRLPGCTHGWQDADGALVGVGAPWPGAPQVRRSIRCLR 180  
Db 121 IINYLGHCSISLVALLVAFVFLFLRLPGCTHGWQDADGALVGVGAPWPGAPQVRRSIRCLR 180  
QY 181 NIIHWNLSAFILRNATFVVLQTMSPVHOSVNGWCRVLTAAAYNFHVTNPFWMFGECC 240  
Db 181 NIIHWNLSAFILRNATFVVLQTMSPVHOSVNGWCRVLTAAAYNFHVTNPFWMFGECC 240  
QY 241 YLHTAIVLTVSTDRLRKWFICIGWVPPPIIYVAAIGKLYYDNEKWCWFKRGKRGVYTDYI 300  
Db 241 YLHTAIVLTVSTDRLRKWFICIGWVPPPIIYVAAIGKLYYDNEKWCWFKRGKRGVYTDYI 300  
QY 301 YQGPMLVLLINFIPLFNIVRIILMTKLRASTTSETIQYKAVKATVLLPLLGITVLMFF 360  
Db 301 YQGPMLVLLINFIPLFNIVRIILMTKLRASTTSETIQYKAVKATVLLPLLGITVLMFF 360  
QY 361 VNPGEDEVSRVVEIYFNFSFLESFGQFVSVFYCFNLSEVRSARIRKRWHRQDKHSIRARV 420  
Db 361 VNPGEDEVSRVVEIYFNFSFLESFGQFVSVFYCFNLSEVRSARIRKRWHRQDKHSIRARV 420  
QY 421 ARAMSIPTSPTRVSRFHSIKOSTAV 444  
Db 421 ARAMSIPTSPTRVSRFHSIKOSTAV 444

RESULT 6  
ID ADE62734 standard; protein; 444 AA.  
XX  
AC ADE62734;  
XX  
XX 29-JAN-2004 (first entry)  
XX  
DE Human Protein P34998, SEQ ID NO 8667.  
XX  
KW Human; pain; neuronal tissue; gene therapy;  
KW spinal segmental nerve injury; chronic constriction injury; CCI;  
KW spared nerve injury; SNI; Chung.  
XX  
OS Homo sapiens.  
XX  
XX WO2003016475-A2.  
XX  
XX 27-FEB-2003.  
XX  
XX 14-AUG-2002; 2002WO-US025765.  
XX  
XX 14-AUG-2001; 2001US-0312147P.  
XX  
XX 01-NOV-2001; 2001US-0346382P.  
XX  
XX 26-NOV-2001; 2001US-0333347P.  
XX  
XX (GEO ) GEN HOSPITAL CORP.  
XX  
XX (FARB ) BAYER AG.  
XX  
XX Woolf C, D'urso D, Befort K, Costigan M;  
XX  
XX WPI; 2003-268312/26.  
XX  
XX GENBANK; P34998.

PT New composition comprising two or more isolated polypeptides, useful for  
PT preparing a medicament for treating pain in an animal.  
XX  
XX Claim 1; Page; 1017pp; English.  
XX  
XX The invention discloses a composition comprising two or more isolated rat  
XX or human polynucleotides or a polynucleotide which represents a fragment,  
XX derivative or allelic variation of the nucleic acid sequence. Also  
XX claimed are a vector comprising the novel polynucleotide, a host cell  
XX comprising the vector, a method for identifying a nucleotide sequence  
XX which is differentially regulated in an animal subjected to pain and a  
XX kit to perform the method, an array, a method for identifying an agent

CC that increases or decreases the expression of the polynucleotide sequence  
CC that is differentially expressed in neuronal tissue of a first animal  
CC subjected to pain, a method for identifying a compound which regulates  
CC the expression of a polynucleotide sequence which is differentially  
CC expressed in an animal subjected to pain, a method for identifying a  
CC compound that regulates the activity of one or more of the  
CC polynucleotides, a method for producing a pharmaceutical composition, a  
CC method for identifying a compound or small molecule that regulates the  
CC activity in an animal of one or more of the polypeptides given in the  
CC specification, a method for identifying a compound useful in treating  
CC pain and a pharmaceutical composition comprising the one or more  
CC polypeptides or their antibodies. The polynucleotide or the compound that  
CC modulates its activity is useful for preparing a medicament for treating  
CC pain (e.g. spinal segmental nerve injury (SNI)), chronic constriction  
CC injury (CCI) and spared nerve injury (SNI) in an animal (e.g. gene  
CC therapy). The sequence presented is a human protein (shown in Table 2 of  
CC the specification) which is differentially expressed during pain. Note:  
CC The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic form directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences.  
XX  
XX Sequence 444 AA;

Query Match 100.0%; Score 2381; DB 7; Length 444;  
Best Local Similarity 100.0%; Pred. No. 8.9e-245;  
Matches 444; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGGHPQLRLVKALLLGLNPNVSASLQDHCEISLASNISGLQCNASVDLIGTCWPRSPA 60  
Db 1 MGGHPQLRLVKALLLGLNPNVSASLQDHCEISLASNISGLQCNASVDLIGTCWPRSPA 60  
QY 61 GQLVVRPCPAFFYGVRYNTTNGYRECLANGSWAARVNSECOEILNEEKSKVHHVAV 120  
Db 61 GQLVVRPCPAFFYGVRYNTTNGYRECLANGSWAARVNSECOEILNEEKSKVHHVAV 120  
QY 121 IINYLGHCSISLVALLVAFVFLFLRLPGCTHGWQDADGALVGVGAPWPGAPQVRRSIRCLR 180  
Db 121 IINYLGHCSISLVALLVAFVFLFLRLPGCTHGWQDADGALVGVGAPWPGAPQVRRSIRCLR 180  
QY 181 NIIHWNLSAFILRNATFVVLQTMSPVHOSVNGWCRVLTAAAYNFHVTNPFWMFGECC 240  
Db 181 NIIHWNLSAFILRNATFVVLQTMSPVHOSVNGWCRVLTAAAYNFHVTNPFWMFGECC 240  
QY 241 YLHTAIVLTVSTDRLRKWFICIGWVPPPIIYVAAIGKLYYDNEKWCWFKRGKRGVYTDYI 300  
Db 241 YLHTAIVLTVSTDRLRKWFICIGWVPPPIIYVAAIGKLYYDNEKWCWFKRGKRGVYTDYI 300  
QY 301 YQGPMLVLLINFIPLFNIVRIILMTKLRASTTSETIQYKAVKATVLLPLLGITVLMFF 360  
Db 301 YQGPMLVLLINFIPLFNIVRIILMTKLRASTTSETIQYKAVKATVLLPLLGITVLMFF 360  
QY 361 VNPGEDEVSRVVEIYFNFSFLESFGQFVSVFYCFNLSEVRSARIRKRWHRQDKHSIRARV 420  
Db 361 VNPGEDEVSRVVEIYFNFSFLESFGQFVSVFYCFNLSEVRSARIRKRWHRQDKHSIRARV 420  
QY 421 ARAMSIPTSPTRVSRFHSIKOSTAV 444  
Db 421 ARAMSIPTSPTRVSRFHSIKOSTAV 444

RESULT 7  
ADJ65810  
ID ADJ65810 standard; protein; 444 AA.  
XX  
XX AC ADJ65810;  
XX  
XX 20-MAY-2004 (first entry)  
XX  
XX Human corticotropin-releasing factor receptor CRF-RA2.  
XX  
XX Human; corticotropin-releasing factor receptor; CRF-RA2; ss; gene;  
KW Alzheimer's disease; melancholic depression; anorexia nervosa;  
KW Cushing's disease; hypercortisolemia; alcoholism;

KW gastrointestinal disorder; irritable bowel syndrome; inflammation;  
 KW Addison's disease; cardiac perfusion; blood pressure; hypotension.  
 XX Homo sapiens.

XX US2004039173-A1.

XX 26-FEB-2004.

XX 26-AUG-2003; 2003US-00649193.

XX 18-JUN-1993; 93US-00079320.

XX 23-AUG-1993; 93US-00110286.

XX 25-MAY-1994; 94MO-US005908.

XX 09-DEC-1994; 94US-00353537.

XX 07-JUN-1995; 95US-00483139.

XX 12-NOV-1998; 98US-00191724.

XX (SALK ) SALK INST BIOLOGICAL STUDIES.

XX Perrin MH, Chen R, Lewis KA, Vale WM, Donaldson CJ, Sawchenko P;

XX WPI; 2004-203293/19.

XX N-PSDB; ADJ65809.

XX New mammalian G protein-coupled corticotropin-releasing factor receptor

XX protein, useful in diagnosing and treating Alzheimer's disease, anorexia

XX nervosa, Cushing's disease, alcoholism, irritable bowel syndrome or

XX hypotension.

XX Claim 7; SEQ ID NO 15; 44pp; English.

XX The invention relates to an isolated mammalian G protein-coupled  
 CC corticotropin-releasing factor (CRF) receptor protein or polypeptide from  
 CC Rat, Mouse or human appearing as ADJ65801, ADJ65803, ADJ65805, or  
 CC ADJ65810, encoded by the nucleic acids appearing as ADJ65800, ADJ65802,  
 CC ADJ65804, or ADJ65809. Also included are a composition comprising CRF-R,  
 CC an antibody generated against CRF-R and a diagnostic kit, for assaying  
 CC for the presence in biological fluids of CRF-R protein, protein analogues  
 CC and/or fragments, comprising CRF-R and/or one or more antibodies. The  
 CC protein, polynucleotide or composition is useful in diagnosing and  
 CC treating Alzheimer's disease, melancholic depression, anorexia nervosa,  
 CC Cushing's disease, hypercortisolemia or alcoholism, gastrointestinal  
 CC disorders (e.g. irritable bowel syndrome) or physiological conditions  
 CC (e.g. inflammation or Addison's disease), in regulating cardiac perfusion  
 CC and in modulating blood pressure, thus combat hypotension. The present  
 CC sequence represents human splice variant CRF-RA2.

XX Sequence 444 AA;

XX Query Match 100.0%; Score 2381; DB 8; Length 444;  
 XX Best Local Similarity 100.0%; Pred. No. 8.9e-245;  
 XX Matches 444; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGGHPQLRLVKALLLGLNPNVSLQDQHCESLSLASNISGLQCNAVLDIGTCWPRSPA 60

DB 1 MGGHPQLRLVKALLLGLNPNVSLQDQHCESLSLASNISGLQCNAVLDIGTCWPRSPA 60

QY 61 GQLVVRPCPAFFYGVRYNTTNGYRECLANGSWAARVNYSECQIILNEEKSKVHYHVAV 120

DB 61 GQLVVRPCPAFFYGVRYNTTNGYRECLANGSWAARVNYSECQIILNEEKSKVHYHVAV 120

QY 121 IINYLGHCLSLVALLVAVFLRLRPGCTHWGDAQDGALEVGAPWPGAPQVRRSRICLR 180

DB 121 IINYLGHCLSLVALLVAVFLRLRPGCTHWGDAQDGALEVGAPWPGAPQVRRSRICLR 180

QY 181 NIHNWNLISAFILRNATFVQVLTMSPEVHQSNVGCRLVTAAYNYFHTNFFMFEQGC 240

DB 181 NIHNWNLISAFILRNATFVQVLTMSPEVHQSNVGCRLVTAAYNYFHTNFFMFEQGC 240

QY 241 YLHTAIVLTYSTDRLRKWNFCICGWGVPFPIIVAMAIGLYDNEKCNFKGKPGVYTDYI 300

DB 241 YLHTAIVLTYSTDRLRKWNFCICGWGVPFPIIVAMAIGLYDNEKCNFKGKPGVYTDYI 300

QY 301 YQGPMLVLLINFIPLFNIVRIILMTKLRASTSETIOYRKAVKATVLLPLIGITVMLFF 360  
 DB 301 YQGPMLVLLINFIPLFNIVRIILMTKLRASTSETIOYRKAVKATVLLPLIGITVMLFF 360  
 QY 361 VNPGEDEVSRVVIYFNFSFLESFQGFVSVFYCFNLSEVRSAIRKRWHRWQDKHSIRARV 420  
 DB 361 VNPGEDEVSRVVIYFNFSFLESFQGFVSVFYCFNLSEVRSAIRKRWHRWQDKHSIRARV 420  
 QY 421 ARAMSIPPTSPTTRVSVFHSIKQSTAV 444  
 DB 421 ARAMSIPPTSPTTRVSVFHSIKQSTAV 444

RESULT 8

ADC86255

ID ADC86255 standard; protein; 447 AA.

XX AC ADC86255;

XX DT 01-JAN-2004 (first entry)

XX DE Human GPCR protein SEQ ID NO:708.

XX KW human; GPCR; guanosine triphosphate-binding protein coupled receptor;

XX KW gene therapy.

XX OS Homo sapiens.

XX PN EP1270724-A2.

XX PD 02-JAN-2003.

XX PF 18-JUN-2002; 2002EP-00013517.

XX PR 18-JUN-2001; 2001JP-00246789.

XX PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.

XX PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.

XX PI Suwa M, Asai K, Akiyama Y, Aburatani H;

XX WPI; 2003-315783/31.

XX DR N-PSDB; ADC86254.

XX PT New polynucleotide, useful for preparing a composition for treating a  
 PT patient in need of increased or suppressed activity or expression of the  
 PT guanosine triphosphate-binding protein coupled receptor.  
 XX Claim 2; SEQ ID NO 708; 28pp; English.

XX The invention relates to a novel polynucleotide encoding a guanosine  
 CC triphosphate-binding protein coupled receptor (GPCR). A polynucleotide of  
 CC the invention may have a use in gene therapy. The polynucleotide and  
 CC polypeptide are useful for preparing a composition for treating a patient  
 CC in need of increased or suppressed activity or expression of the  
 CC guanosine triphosphate-binding protein coupled receptor. The protein  
 CC sequences shown in ADC85549-ADC87617 represent GPCR's of the invention.

XX Sequence 447 AA;

XX Query Match 97.6%; Score 2324; DB 7; Length 447;  
 XX Best Local Similarity 99.8%; Pred. No. 1.1e-238;  
 XX Matches 433; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 11 KALLLGLNPNVSLQDQHCESLSLASNISGLQCNAVLDIGTCWPRSPAGQLVVRPCPA 70

DB 14 RALLLGLNPNVSLQDQHCESLSLASNISGLQCNAVLDIGTCWPRSPAGQLVVRPCPA 73

QY 71 PFYGVRYNTTNGYRECLANGSWAARVNYSECQIILNEEKSKVHYHVAVIINYLGHCLIS 130

DB 74 PFYGVRYNTTNGYRECLANGSWAARVNYSECQIILNEEKSKVHYHVAVIINYLGHCLIS 133



QY 131 LVALLVAFVFLRLRPGCTHWGDAQDGALEVGAPWVGAPVQVRSSIRCLNIIHWNLSA 190  
 DB 134 LVALLVAFVFLRLRPGCTHWGDAQDGALEVGAPWVGAPVQVRSSIRCLNIIHWNLSA 193  
 QY 191 FILRNATFWVQVLTMSPEVHQSNVGCRLVTAAYNYPHVTNFFWFMGEGCYLHTAIVLTY 250  
 DB 194 FILRNATFWVQVLTMSPEVHQSNVGCRLVTAAYNYPHVTNFFWFMGEGCYLHTAIVLTY 253  
 QY 251 STDRLRKWMEFCIGWGVPPPIIIVAWAIGKLYDYNEKWCWFGKRGVYTDYIYQGPMLVLL 310  
 DB 254 STDRLRKWMEFCIGWGVPPPIIIVAWAIGKLYDYNEKWCWFGKRGVYTDYIYQGPMLVLL 313  
 QY 311 INFILFNIIVRIILMTKLRASTTSETIOYRKAVKATLVLLPILGITYMLPFVNFGEDVSR 370  
 DB 314 INFILFNIIVRIILMTKLRASTTSETIOYRKAVKATLVLLPILGITYMLPFVNFGEDVSR 373  
 QY 371 VFIYFNSFLESFGQFPVSVFYCFNLSEVRSALKRWHRQDQKHSIRARVARAMSPTSP 430  
 DB 374 VFIYFNSFLESFGQFPVSVFYCFNLSEVRSALKRWHRQDQKHSIRARVARAMSPTSP 433  
 QY 431 TRVSFHSIKOSTAV 444  
 DB 434 TRVSFHSIKOSTAV 447

RESULT 9  
 AAR69519  
 ID AAR69519 standard; protein; 415 AA.  
 XX AAR69519;  
 AC AAR69519;  
 XX AAR69519;  
 DT 25-MAR-2003 (revised)  
 DT 21-AUG-1995 (first entry)  
 XX  
 DE Human pituitary corticotropin releasing factor receptor CRF-R1.  
 XX  
 XX Pituitary; hormone; corticotropin releasing factor receptor;  
 KW hypothalamus; adencorticotrophic hormone; ACTH; Cushing's disease;  
 KW pituitary tumor; diagnosis.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key  
 FT Modified-site 38 Location/Qualifiers  
 FT /note= "glycosylation site"  
 FT Modified-site 45  
 FT /note= "glycosylation site"  
 FT Modified-site 78  
 FT /note= "glycosylation site"  
 FT Modified-site 90  
 FT /note= "glycosylation site"  
 FT Modified-site 98  
 FT /note= "glycosylation site"  
 FT Modified-site 146  
 FT /note= "protein-kinase-C phosphorylation site"  
 FT Modified-site 222  
 FT /note= "protein-kinase-C phosphorylation site"  
 FT Modified-site 301  
 FT /note= "casein-kinase-II phosphorylation site"  
 FT Modified-site 302  
 FT /note= "protein-kinase-A phosphorylation site"  
 FT Modified-site 386  
 FT /note= "protein-kinase-C phosphorylation site"  
 FT Modified-site 408  
 FT /note= "protein-kinase-C phosphorylation site"  
 XX  
 PN WO9500640-A1.  
 XX  
 PD 05-JAN-1995.  
 XX  
 PP 25-MAY-1994; 94WO-US005908.  
 XX  
 PR 18-JUN-1993; 93US-00079320.  
 XX

PR 23-AUG-1993; 93US-00110286.  
 XX (SALK ) SALK INST BIOLOGICAL STUDIES.  
 XX  
 PI Perrin MH, Chen R, Lewis KA, Vale WW, Donaldson CJ;  
 XX  
 DR WPI; 1995-052077/07.  
 DR N-PSDB; AAQ81952.  
 XX  
 XX Isolated corticotropin releasing factor receptor and nucleic acid - also  
 PT antibodies, useful for diagnosis and treatment of Cushing's disease,  
 PT pituitary tumours etc., also to identify specific agonists and  
 PT antagonists.  
 XX  
 PS Claim 3; Page 65; 84pp; English.  
 XX  
 CC This protein can be used to determine CRF (e.g. over- or under-  
 CC production, high levels of CRF late in pregnancy may indicate risk of  
 CC premature labor). Cells expressing the protein are used to identify e.g.  
 CC antibodies, which can be used to modulate signal transduction activity.  
 CC  
 CC mediated by CRF receptors. Typical applications are in the treatment of  
 CC Cushing's disease, pituitary tumors, etc. (Updated on 25-MAR-2003 to  
 CC correct PN field.)  
 XX  
 SQ Sequence 415 AA;  
 CC  
 Query Match 91.8%; Score 2186.5; DB 2; Length 415;  
 Best Local Similarity 93.5%; Pred. No. 4.8e-224;  
 Matches 415; Conservative 0; Mismatches 0; Indels 29; Gaps 1;  
 QY 1 MCGHPQLRLVKALLGLNPVSASLQDHCESLSLASNISGLQCNASVDLIGTCWPRSPA 60  
 DB 1 MCGHPQLRLVKALLGLNPVSASLQDHCESLSLASNISGLQCNASVDLIGTCWPRSPA 60  
 QY 61 GQLVVRPCPAFFYGVRYNTNNGYRECLANGSWAARVNYSECOEILNEEKSKVHVAV 120  
 DB 61 GQLVVRPCPAFFYGVRYNTNNGYRECLANGSWAARVNYSECOEILNEEKSKVHVAV 120  
 QY 121 IINYLGHICISLVALVAFVFLRLRPGCTHWGDAQDGALEVGAPWVGAPVQVRSSIRCLR 180  
 DB 121 IINYLGHICISLVALVAFVFLRLRPGCTHWGDAQDGALEVGAPWVGAPVQVRSSIRCLR 180  
 QY 181 NIIHWNLSAFILRNATFWVQVLTMSPEVHQSNVGCRLVTAAYNYPHVTNFFWFMGEGC 240  
 DB 152 NIIHWNLSAFILRNATFWVQVLTMSPEVHQSNVGCRLVTAAYNYPHVTNFFWFMGEGC 211  
 QY 241 YLHTAIVLTYSTDRLRKWMEFCIGWGVPPPIIIVAWAIGKLYDYNEKWCWFGKRGVYTDYI 300  
 DB 212 YLHTAIVLTYSTDRLRKWMEFCIGWGVPPPIIIVAWAIGKLYDYNEKWCWFGKRGVYTDYI 271  
 QY 301 YQGPMLVLLINFILFNIIVRIILMTKLRASTTSETIOYRKAVKATLVLLPILGITYMLFF 360  
 DB 272 YQGPMLVLLINFILFNIIVRIILMTKLRASTTSETIOYRKAVKATLVLLPILGITYMLFF 331  
 QY 361 VNPGEDEVSRVFIYFNSFLESFGQFPVSVFYCFNLSEVRSALKRWHRQDQKHSIRARV 420  
 DB 332 VNPGEDEVSRVFIYFNSFLESFGQFPVSVFYCFNLSEVRSALKRWHRQDQKHSIRARV 391  
 QY 421 ARAMSIPTSPTVRSPHSIKOSTAV 444  
 DB 392 ARAMSIPTSPTVRSPHSIKOSTAV 415

RESULT 10  
 AAR97290  
 ID AAR97290 standard; protein; 415 AA.  
 XX AAR97290;  
 AC AAR97290;  
 XX  
 DT 21-AUG-1996 (first entry)  
 XX  
 DE Human CRF receptor CRF-R1.  
 XX

KW Corticotropin releasing factor receptor; CRF-R; corticoliberin;  
 XX signal transduction.

OS Homo sapiens.

XX Key Location/Qualifiers

FT Modified-site 38 /label= N-glycosylation\_site

FT Modified-site 45 /label= N-glycosylation\_site

FT Modified-site 78 /label= N-glycosylation\_site

FT Modified-site 90 /label= N-glycosylation\_site

FT Modified-site 98 /label= N-glycosylation\_site

FT Modified-site 146 /label= N-glycosylation\_site

FT Modified-site 222 /label= Phosphorylation site

FT Modified-site 301 /label= "protein kinase C phosphorylation site"

FT Modified-site 302 /label= "protein kinase II phosphorylation site"

FT Modified-site 386 /label= "protein kinase A phosphorylation site"

FT Modified-site 408 /label= "protein kinase C phosphorylation site"

FT Modified-site /label= "protein kinase C phosphorylation site"

FT Modified-site /label= "protein kinase C phosphorylation site"

FT Modified-site /label= "protein kinase C phosphorylation site"

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FT Modified-site /label= "protein kinase C phosphorylation site"

QY 1 MGHGPOLRLVKALLLGLNPVSASLQDQHCESLSLASNISGLQCNASVDLIGTCWPRSPA 60  
 DB 1 MGHGPOLRLVKALLLGLNPVSASLQDQHCESLSLASNISGLQCNASVDLIGTCWPRSPA 60  
 QY 61 GQLVVRPCPAFFYGVRYNTTNGYRECLANGSWAARVNYSECQEIINEEKKSKVHYHVA 120  
 DB 61 GQLVVRPCPAFFYGVRYNTTNGYRECLANGSWAARVNYSECQEIINEEKKSKVHYHVA 120  
 QY 121 IINYLGHCSISVALLVAFVLFLRLPCTHWDGADGALVPGWGAFFQVRRSTRICLR 180  
 DB 121 IINYLGHCSISVALLVAFVLFLRLPCTHWDGADGALVPGWGAFFQVRRSTRICLR 180  
 QY 181 NIIHWNLIISAFILRNATFWVOLTMSPEVHQSNVGMCRVLTAAVYFHVTFNFMFGECC 240  
 DB 181 NIIHWNLIISAFILRNATFWVOLTMSPEVHQSNVGMCRVLTAAVYFHVTFNFMFGECC 240  
 QY 241 YLHTAIVLTYSTDLRLKMMFICIGWGVPPPIIVAMAIGKLYYDNEKWCNFKGPGVYTDYI 300  
 DB 241 YLHTAIVLTYSTDLRLKMMFICIGWGVPPPIIVAMAIGKLYYDNEKWCNFKGPGVYTDYI 300  
 QY 301 YQGPMLIVLLINFIPLFNIVRIIMTKLRASITSETIOYRKAVKATLVLLPLIGITVMLFP 360  
 DB 301 YQGPMLIVLLINFIPLFNIVRIIMTKLRASITSETIOYRKAVKATLVLLPLIGITVMLFP 360  
 QY 361 VNPGEDEVSRVVFYFNSFLESFQGFVSVFYCFNLSEVRSAIRKRWQDKHSIRARV 420  
 DB 361 VNPGEDEVSRVVFYFNSFLESFQGFVSVFYCFNLSEVRSAIRKRWQDKHSIRARV 420  
 QY 421 ARAMSIPTSPTRVSPHSIKQSTAV 444  
 DB 421 ARAMSIPTSPTRVSPHSIKQSTAV 444  
 QY 444 ARAMSIPTSPTRVSPHSIKQSTAV 415  
 DB 444 ARAMSIPTSPTRVSPHSIKQSTAV 415  
 RESULT 11  
 AAW00159  
 ID AAW00159 standard; protein; 415 AA.  
 XX  
 AC AAW00159;  
 XX  
 DT 16-OCT-1996 (first entry)  
 XX  
 DE Human corticotropin releasing factor receptor protein.  
 XX  
 KW Human; corticotropin releasing factor; CRF; receptor; expression vector;  
 KW pAC02; agonist; antagonist; blood pressure; immunosuppression.  
 XX  
 OS Homo sapiens.  
 XX  
 PN JP08140680-A.  
 XX  
 PD 04-JUN-1996.  
 XX  
 PF 22-NOV-1994; 94JP-00287638.  
 XX  
 PR 22-NOV-1994; 94JP-00287638.  
 XX  
 PA (TAKE ) TAKEDA CHEM IND LTD.  
 XX  
 DR WPI; 1996-316316/32.  
 DR N-PSDB; AAT37068.  
 XX  
 PT Recombinant human corticotropin releasing factor receptor protein -  
 PT useful to screen for (ant)agonist for lowering blood pressure, as a  
 PT gastrointestinal regulator and for treatment of immunosuppression.  
 XX  
 PS Claim 1; Fig 1; 21pp; Japanese.  
 XX  
 CC This sequence represents human corticotropin releasing factor (CRF)  
 CC receptor protein. The cDNA fragment is derived from the expression vector  
 CC designated pAC02. pAC02 is an expression vector constructed for elevated  
 CC expression of the human CRF receptor protein. The recombinantly produced  
 CC CRF receptor protein or a peptide fragment, may be used for efficient and  
 CC rapid screening of an agonist or antagonist of human CRF receptor.

XX Sequence 415 AA;

Query Match 91.8%; Score 2186.5; DB 2; Length 415;

Best Local Similarity 93.5%; Pred. No. 4.8e-224;

Matches 415; Conservative 0; Mismatches 0; Indels 29; Gaps 1;

XX Isolated corticotropin-releasing factor receptor (CRF-R) - used to  
 develop prods. for modulating signal transduction activity mediated by  
 CRF-R.

XX Claim 3; Page 75-77; 102pp; English.

XX A new G-protein-coupled receptor protein, CRF-R1 (AAR97290), has high  
 CC binding affinity for corticotropin releasing factor (CRF). The amino acid  
 CC sequence was deduced from a cDNA clone (AAT28968) isolated from human  
 CC pituitary corticotrope adenoma (Cushing's tumour). This cDNA can be used  
 CC for prodn. of recombinant CRF-R1. A splice variant contg. a 29-amino acid  
 CC insert (AAR97291) was also identified. The receptor can be used to  
 CC identify agonists and antagonists that modulate the signal transduction  
 CC activity mediated by CRF receptors. The receptor can be administered  
 CC therapeutically to reduce high ACTH levels caused by excess CRF

CC Agonists may be used for lowering blood pressure, and antagonists may be  
CC used for the treatment of immunosuppression  
XX  
SQ Sequence 415 AA;

Query Match 91.8%; Score 2186.5; DB 2; Length 415;  
Best Local Similarity 93.5%; Pred. No. 4.8e-224;  
Matches 415; Conservative 0; Mismatches 0; Indels 29; Gaps 1;  
1 MGGHPQLRLVKALLLGLNLPVSASLQDQHCHCESLSLASNISGLQCNASVDLIGTCWPRSPA 60  
Db 1 MGGHPQLRLVKALLLGLNLPVSASLQDQHCHCESLSLASNISGLQCNASVDLIGTCWPRSPA 60  
Qy 61 GQLVVRPCPAFFYGVRYNTTNGYRECLANGSWAARVNYSECQEIILNEEKSKVHHVAV 120  
Db 61 GQLVVRPCPAFFYGVRYNTTNGYRECLANGSWAARVNYSECQEIILNEEKSKVHHVAV 120  
Qy 121 IINYLGHCSLVALLVAFVFLRLRPGCTHWGDAQDGALEVGAPWSPAPQVRRSIRCLR 180  
Db 121 IINYLGHCSLVALLVAFVFLRLR-----RSIRCLR 151  
Qy 181 NIIHWNLSAFILRNATFWVQLTMSPEVHQSNVGMCRLVTAAYNYFHVTFNFFMFGEGC 240  
Db 152 NIIHWNLSAFILRNATFWVQLTMSPEVHQSNVGMCRLVTAAYNYFHVTFNFFMFGEGC 211  
Qy 241 YLHTAIVLTYSTDRLRKWMPICIGWGPVPIIIVAWAIGKLYYDNEKCFKRGVYTDYI 300  
Db 212 YLHTAIVLTYSTDRLRKWMPICIGWGPVPIIIVAWAIGKLYYDNEKCFKRGVYTDYI 271  
Qy 301 YQGPMLVLLINFIPLNIVRIILMTKLRASTTSETIOYRKAVKATLVLLPLLGITYMLFF 360  
Db 272 YQGPMLVLLINFIPLNIVRIILMTKLRASTTSETIOYRKAVKATLVLLPLLGITYMLFF 331  
Qy 361 VNPGEDEVSRVFIYFNSFLESFGFVSVFYCFLNSEVRSAIRKRWHRWQDKHSIRARV 420  
Db 332 VNPGEDEVSRVFIYFNSFLESFGFVSVFYCFLNSEVRSAIRKRWHRWQDKHSIRARV 391  
Qy 421 ARAMSIPTSPTRVSHSIKOSTAV 444  
Db 392 ARAMSIPTSPTRVSHSIKOSTAV 415

RESULT 12  
AAE26679  
ID AAE26679 standard; protein; 415 AA.  
AC AAE26679;  
XX  
DT 13-DEC-2002 (first entry)  
DE Human CRF-RA1 protein.  
XX  
KW Human; G protein-coupled corticotropin-releasing factor receptor; CRF;  
KW CRF-R; adrenocorticotrophic hormone; irritable bowel syndrome; therapy;  
KW Cushing's syndrome; pituitary tumour; chronic stress; anorexia nervosa;  
KW receptor; alcoholism; CRF-RA1.  
XX  
OS Homo sapiens.  
XX  
PN US2002055617-A1.  
PD  
XX 09-MAY-2002.  
XX 12-NOV-1998; 98US-00191724.  
XX 18-JUN-1993; 93US-00079320.  
PR 23-AUG-1993; 93US-00110286.  
PR 25-MAY-1994; 94WO-US005908.  
PR 09-DEC-1994; 94US-00353537.  
PR 07-JUN-1995; 95US-00483139.  
XX  
XX (PERR/) PERRIN M H.  
PA (CHEN/) CHEN R.

PA (LEWI/) LEWIS X A.  
PA (VALE/) VALE W W.  
PA (DONA/) DONALDSON C J.  
PA (SAWC/) SAWCHENKO P.  
XX  
PI Perrin MH, Chen R, Lewis KA, Vale WW, Donaldson CJ, Sawchenko P;  
XX WPI; 2002-462916/49.  
DR N-PSDB; AAD44482.  
XX  
XX New isolated recombinant mammalian G protein-coupled corticotropin-  
PT releasing factor receptor protein for treating e.g. Cushing's syndrome,  
PT pituitary tumors, stress, anorexia, alcoholism or irritable bowel  
PT syndrome.  
XX  
PS Claim 4; Page 22-23; 44pp; English.  
XX  
XX The invention relates to recombinant mammalian G protein-coupled  
CC corticotropin-releasing factor (CRF) receptor (CRF-R) proteins having  
CC high affinity for CRF and nucleic acid molecules encoding such receptor  
CC proteins. Polypeptides of the invention can be used to reduce high levels  
CC of adrenocorticotrophic hormone caused by excess CRF and so can be used  
CC to treat diseases such as Cushing's syndrome, pituitary tumours, chronic  
CC stress, anorexia nervosa, alcoholism and irritable bowel syndrome. They  
CC are used in pharmaceuticals and in the production of antibodies. The  
CC present sequence is human CRF-RA1 protein  
XX  
SQ Sequence 415 AA;

Query Match 91.8%; Score 2186.5; DB 5; Length 415;  
Best Local Similarity 93.5%; Pred. No. 4.8e-224;  
Matches 415; Conservative 0; Mismatches 0; Indels 29; Gaps 1;  
1 MGGHPQLRLVKALLLGLNLPVSASLQDQHCHCESLSLASNISGLQCNASVDLIGTCWPRSPA 60  
Db 1 MGGHPQLRLVKALLLGLNLPVSASLQDQHCHCESLSLASNISGLQCNASVDLIGTCWPRSPA 60  
Qy 61 GQLVVRPCPAFFYGVRYNTTNGYRECLANGSWAARVNYSECQEIILNEEKSKVHHVAV 120  
Db 61 GQLVVRPCPAFFYGVRYNTTNGYRECLANGSWAARVNYSECQEIILNEEKSKVHHVAV 120  
Qy 121 IINYLGHCSLVALLVAFVFLRLRPGCTHWGDAQDGALEVGAPWSPAPQVRRSIRCLR 180  
Db 121 IINYLGHCSLVALLVAFVFLRLR-----RSIRCLR 151  
Qy 181 NIIHWNLSAFILRNATFWVQLTMSPEVHQSNVGMCRLVTAAYNYFHVTFNFFMFGEGC 240  
Db 152 NIIHWNLSAFILRNATFWVQLTMSPEVHQSNVGMCRLVTAAYNYFHVTFNFFMFGEGC 211  
Qy 241 YLHTAIVLTYSTDRLRKWMPICIGWGPVPIIIVAWAIGKLYYDNEKCFKRGVYTDYI 300  
Db 212 YLHTAIVLTYSTDRLRKWMPICIGWGPVPIIIVAWAIGKLYYDNEKCFKRGVYTDYI 271  
Qy 301 YQGPMLVLLINFIPLNIVRIILMTKLRASTTSETIOYRKAVKATLVLLPLLGITYMLFF 360  
Db 272 YQGPMLVLLINFIPLNIVRIILMTKLRASTTSETIOYRKAVKATLVLLPLLGITYMLFF 331  
Qy 361 VNPGEDEVSRVFIYFNSFLESFGFVSVFYCFLNSEVRSAIRKRWHRWQDKHSIRARV 420  
Db 332 VNPGEDEVSRVFIYFNSFLESFGFVSVFYCFLNSEVRSAIRKRWHRWQDKHSIRARV 391  
Qy 421 ARAMSIPTSPTRVSHSIKOSTAV 444  
Db 392 ARAMSIPTSPTRVSHSIKOSTAV 415

RESULT 13  
AAO19420  
ID AAO19420 standard; protein; 415 AA.  
XX  
XX AAO19420;  
XX  
XX 10-DEC-2002 (first entry)  
DT

XX DE Human corticotrophin releasing factor receptor CRF1R.  
 XX KW Human; rat; mouse; sheep; cow; chicken; CRF1R; CRF2R;  
 KW skeletal muscle atrophy; corticotrophin releasing factor-2 receptor;  
 KW muscular dystrophy; corticotrophin releasing factor-1 receptor;  
 KW gene therapy.  
 XX KW Homo sapiens.  
 XX PN WO200269908-A2.  
 XX PD 12-SEP-2002.  
 XX PF 06-MAR-2002; 2002WO-US0007476.  
 XX PR 06-MAR-2001; 2001US-00799978.  
 XX PA (PROC ) PROCTER & GAMBLE CO.  
 XX PI Isfort RJ, Sheldon RJ;  
 XX DR WPI; 2002-713413/77.  
 XX DR N-PSDB; AAL49971.  
 XX PT Identifying candidate compounds for regulating skeletal muscle mass or  
 PT treating skeletal muscle atrophy by identifying test compounds that bind  
 PT to, or activate, the corticotrophin releasing factor-2 receptor.  
 XX PS Disclosure; Page 79-80; 167pp; English.  
 XX CC The present invention relates to a method of identifying candidate  
 CC compounds for regulating skeletal muscle mass or function, and comprises  
 CC contacting a test compound with a corticotropin releasing factor-2  
 CC receptor (CRF2R) or with a cell expressing a functional CRF2R,  
 CC determining whether the test compound binds to, or activates, the CRF2R  
 CC and identifying the test compounds that bind to, or activates, the CRF2R  
 CC as candidate compounds for regulating skeletal muscle mass or function.  
 CC The method is useful for preparing a medicament for treating skeletal  
 CC muscle atrophy or for prophylactic treatment of muscular dystrophies. The  
 CC present sequence is a corticotrophin releasing factor receptor  
 XX SQ Sequence 415 AA;  
 Query Match 91.8%; Score 2186.5; DB 5; Length 415;  
 Best Local Similarity 93.5%; Pred. No. 4.8e-224;  
 Matches 415; Conservative 0; Mismatches 0; Indels 29; Gaps 1;  
 QY 1 MGHPQLRLVKALLLGLNPNVASLQDQHCESLSLASNISGLQCNASVDLIGTCWPRSPA 60  
 DB 1 MGHPQLRLVKALLLGLNPNVASLQDQHCESLSLASNISGLQCNASVDLIGTCWPRSPA 60  
 QY 61 GQLVVRPCPAFFGVRYNTTNGVRECLANGSWAARVNYSECQIILNEEKSKVHYHVAV 120  
 DB 61 GQLVVRPCPAFFGVRYNTTNGVRECLANGSWAARVNYSECQIILNEEKSKVHYHVAV 120  
 QY 121 IINYLGHICISLVALLVAFVLFLRLPCTHWGDAQDGALEVPWPGAPQVRRSIRCLR 180  
 DB 121 IINYLGHICISLVALLVAFVLFLRLPCTHWGDAQDGALEVPWPGAPQVRRSIRCLR 151  
 QY 181 NIHWNLISAFILRNATWVFVQLTMSPEVHQSNGWCRVLTAAVYFVHTNFTFWMFGECC 240  
 DB 152 NIHWNLISAFILRNATWVFVQLTMSPEVHQSNGWCRVLTAAVYFVHTNFTFWMFGECC 211  
 QY 241 YLHTAIVLTSTDRLRKMMFICIGWGPFPFIIVAWAIGKLYDNEKCMFKRGVYTDYI 300  
 DB 212 YLHTAIVLTSTDRLRKMMFICIGWGPFPFIIVAWAIGKLYDNEKCMFKRGVYTDYI 271  
 QY 301 YQSPMLVLLINIFLNIYRIILMTKLRASTTSETIYRKAVKATVLLPLLGITVMLFF 360  
 DB 272 YQSPMLVLLINIFLNIYRIILMTKLRASTTSETIYRKAVKATVLLPLLGITVMLFF 331  
 QY 361 VNPGEDEVSRVVFYFNSFLESFQGFVSVFYCFNLSEVRSAIRKRWHRWQDKHSIRARV 420

DB 332 VNPGEDEVSRVVFYFNSFLESFQGFVSVFYCFNLSEVRSAIRKRWHRWQDKHSIRARV 391  
 QY 421 ARAMSIPTSPTRVSPHSIKQSTAV 444  
 DB 392 ARAMSIPTSPTRVSPHSIKQSTAV 415  
 RESULT 14  
 AAO19421  
 ID AAO19421 standard; protein; 415 AA.  
 XX AC AAO19421;  
 XX DT 10-DEC-2002 (first entry)  
 XX DE Human corticotrophin releasing factor receptor CRF1R variant.  
 XX KW Human; rat; mouse; sheep; cow; chicken; CRF1R; CRF2R;  
 KW skeletal muscle atrophy; corticotrophin releasing factor-2 receptor;  
 KW muscular dystrophy; corticotrophin releasing factor-1 receptor;  
 KW Gene therapy.  
 XX OS Homo sapiens.  
 XX PN WO200269908-A2.  
 XX PD 12-SEP-2002.  
 XX PF 06-MAR-2002; 2002WO-US0007476.  
 XX PR 06-MAR-2001; 2001US-00799978.  
 XX PA (PROC ) PROCTER & GAMBLE CO.  
 XX PI Isfort RJ, Sheldon RJ;  
 XX DR WPI; 2002-713413/77.  
 XX DR N-PSDB; AAL49972.  
 XX PT Identifying candidate compounds for regulating skeletal muscle mass or  
 PT treating skeletal muscle atrophy by identifying test compounds that bind  
 PT to, or activate, the corticotropin releasing factor-2 receptor.  
 XX PS Disclosure; Page 83-84; 167pp; English.  
 XX CC The present invention relates to a method of identifying candidate  
 CC compounds for regulating skeletal muscle mass or function, and comprises  
 CC contacting a test compound with a corticotropin releasing factor-2  
 CC receptor (CRF2R) or with a cell expressing a functional CRF2R,  
 CC determining whether the test compound binds to, or activates, the CRF2R  
 CC and identifying the test compounds that bind to, or activates, the CRF2R  
 CC as candidate compounds for regulating skeletal muscle mass or function.  
 CC The method is useful for preparing a medicament for treating skeletal  
 CC muscle atrophy or for prophylactic treatment of muscular dystrophies. The  
 CC present sequence is a corticotrophin releasing factor receptor  
 XX SQ Sequence 415 AA;  
 Query Match 91.8%; Score 2186.5; DB 5; Length 415;  
 Best Local Similarity 93.5%; Pred. No. 4.8e-224;  
 Matches 415; Conservative 0; Mismatches 0; Indels 29; Gaps 1;  
 QY 1 MGHPQLRLVKALLLGLNPNVASLQDQHCESLSLASNISGLQCNASVDLIGTCWPRSPA 60  
 DB 1 MGHPQLRLVKALLLGLNPNVASLQDQHCESLSLASNISGLQCNASVDLIGTCWPRSPA 60  
 QY 61 GQLVVRPCPAFFGVRYNTTNGVRECLANGSWAARVNYSECQIILNEEKSKVHYHVAV 120  
 DB 61 GQLVVRPCPAFFGVRYNTTNGVRECLANGSWAARVNYSECQIILNEEKSKVHYHVAV 120  
 QY 121 IINYLGHICISLVALLVAFVLFLRLPCTHWGDAQDGALEVPWPGAPQVRRSIRCLR 180

Db 121 IINVLGHICISLVALLVAFVLFRL-----RSIRCLR 151  
Qy 181 NIIHWNLSAIFILRNATWFFVQVLTMSPEVHQSNGVWCLRTAAAYNYFHVTFNFMFGEGC 240  
Db 152 NIIHWNLSAIFILRNATWFFVQVLTMSPEVHQSNGVWCLRTAAAYNYFHVTFNFMFGEGC 211  
Qy 241 YLHTAIVLTYSTDLRLKWMFCIGWGVPPFIIVAWAIGKLYDNEKCFWGRPGVYTDYI 300  
Db 212 YLHTAIVLTYSTDLRLKWMFCIGWGVPPFIIVAWAIGKLYDNEKCFWGRPGVYTDYI 271  
Qy 301 YQGPMLVLLINFIPLFNIVIRILMTKLRASTTSETIOYRKAVKATLVLLPLLGITYMLFF 360  
Db 272 YQGPMLVLLINFIPLFNIVIRILMTKLRASTTSETIOYRKAVKATLVLLPLLGITYMLFF 331  
Qy 361 VNFGEDEVSRVVIYFNFSFLESFGQFVSVFYCFNLSEVRSAIRKRWHRWQDKHSIRARV 420  
Db 332 VNFGEDEVSRVVIYFNFSFLESFGQFVSVFYCFNLSEVRSAIRKRWHRWQDKHSIRARV 391  
Qy 421 ARAMSIPTSPTRVSEHSIKOSTAV 444  
Db 392 ARAMSIPTSPTRVSEHSIKOSTAV 415

## RESULT 15

ABG66957  
ID ABG66957 standard; protein; 415 AA.

XX AC ABG66957;

XX DT 24-SEP-2002 (first entry)

XX DE Human corticotrophin releasing hormone.

XX KW Yeast; G-Protein Coupled Receptor; GPCR-regulated signaling pathway;  
KW GPCR; sxa2 promoter; Galpha-transplant; Galphaq; Galphas; Galphao;  
KW Galphai2; Galphai3; Galphaz; Galphai2; Galphai3; Galphai4; Galphai6;  
KW receptor.

XX OS Homo sapiens.

XX PN W0200246369-A2.

XX XX 13-JUN-2002.

XX PF 10-DEC-2001; 2001WO-GB005460.

XX PR 08-DEC-2000; 2000GB-00030038.

XX PA (SEPT-) SEPTGEN LTD.

XX PI Davey J;

XX DR WPI; 2002-508557/54.

XX DR N-PSDB; ABK95583.

XX PT New Schizosaccharomyces pombe cell, useful for studying G-protein coupled  
PT receptor-regulated activity, comprises receptor-regulated signaling  
PT pathway that is derepressed during cell growth mitotic phase and  
PT reporter.

XX PS Disclosure; Page 85-87; 117pp; English.

XX CC The invention relates to a Schizosaccharomyces pombe yeast cell (1)  
CC comprising: (a) a heterologous G-Protein Coupled Receptor (GPCR)-  
CC regulated signaling pathway (P1) which is derepressed during mitotic  
CC phase of cell growth; and (b) a reporter system (RS) for reporting signal  
CC mediated by P1, where RS has reporter gene (G1) operatively linked to  
CC promoter (PR), which is regulatable by GPCR, and G1 and PR is  
CC heterologous. Also described is (1) an isolated polynucleotide (Iia)  
CC comprising an sxa2 promoter, or its homologue or analogue, operatively  
CC linked to an exogenous reporter gene; (2) an isolated polynucleotide  
CC (Iib) encoding a Galpha-transplant having a nucleotide sequence from  
CC Galphaq, Galphas, Galphao, Galphai2, Galphai3, Galphaz, Galphai2,

CC Galphai3, Galphai4 and Galphai6. (1), (Iia) or (Iib) is useful for  
CC studying GPCR-regulated activity, for determining the effect of a  
CC compound on GPCR-regulated activity by introducing the compound, to (1)  
CC and noting the output of RS, where the compound affects the ability of  
CC orphan GPCR to regulate RS. Furthermore (1) is useful for identifying a  
CC regulator or a mutant of a component of GPCR-regulated pathway and for  
CC identifying a reagent that modulates GPCR-regulated signaling pathways,  
CC by producing a random peptide within (1) and measuring an amount of  
CC reporter activity produced. ABK95570-ABK95608 represent Galpha-  
CC transplant amino acid sequences and related amino acid sequences of the  
CC invention

XX SQ Sequence 415 AA;

Query Match 91.8%; Score 2186.5; DB 5; Length 415;

Best Local Similarity 93.5%; Pred. No. 4.8e-224;

Matches 415; Conservative 0; Mismatches 0; Indels 29; Gaps 1;

Qy 1 MGGHPQLRLVKALLLGLNPNVSASLODOHCESLSLASNISGLQCNASVDLIGTCWPRSPA 60  
Db 1 MGGHPQLRLVKALLLGLNPNVSASLODOHCESLSLASNISGLQCNASVDLIGTCWPRSPA 60  
Qy 61 GOLVVRPCPAFFYGVRYNTTNGYRECLANGSWAARVNYSECQILNEEKSKVHYHVAV 120  
Db 61 GOLVVRPCPAFFYGVRYNTTNGYRECLANGSWAARVNYSECQILNEEKSKVHYHVAV 120  
Qy 121 IINVLGHICISLVALLVAFVLFRL-----RSIRCLR 180  
Db 121 IINVLGHICISLVALLVAFVLFRL-----RSIRCLR 151  
Qy 181 NIIHWNLSAIFILRNATWFFVQVLTMSPEVHQSNGVWCLRTAAAYNYFHVTFNFMFGEGC 240  
Db 152 NIIHWNLSAIFILRNATWFFVQVLTMSPEVHQSNGVWCLRTAAAYNYFHVTFNFMFGEGC 211  
Qy 241 YLHTAIVLTYSTDLRLKWMFCIGWGVPPFIIVAWAIGKLYDNEKCFWGRPGVYTDYI 300  
Db 212 YLHTAIVLTYSTDLRLKWMFCIGWGVPPFIIVAWAIGKLYDNEKCFWGRPGVYTDYI 271  
Qy 301 YQGPMLVLLINFIPLFNIVIRILMTKLRASTTSETIOYRKAVKATLVLLPLLGITYMLFF 360  
Db 272 YQGPMLVLLINFIPLFNIVIRILMTKLRASTTSETIOYRKAVKATLVLLPLLGITYMLFF 331  
Qy 361 VNFGEDEVSRVVIYFNFSFLESFGQFVSVFYCFNLSEVRSAIRKRWHRWQDKHSIRARV 420  
Db 332 VNFGEDEVSRVVIYFNFSFLESFGQFVSVFYCFNLSEVRSAIRKRWHRWQDKHSIRARV 391  
Qy 421 ARAMSIPTSPTRVSEHSIKOSTAV 444  
Db 392 ARAMSIPTSPTRVSEHSIKOSTAV 415

Search completed: March 16, 2006, 17:16:18

Job time : 195 secs

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GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: March 16, 2006, 17:16:39 ; Search time 41 Seconds  
(without alignments)  
1041.957 Million cell updates/sec

Title: US-10-649-193-15  
Perfect score: 2381  
Sequence: 1 MGHPPQLRLVKALLLLGLNP.....SIPTSPTRVSPHSIKQSTAV 444

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 80.\*

1: pir1.\*

2: pir2.\*

3: pir3.\*

4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2381	100.0	444	2 A48260	corticoliberin rec
2	2137.5	89.8	415	2 S39535	corticotropin-rele
3	2126.5	89.3	415	2 I58144	corticotropin-rele
4	1925.5	80.9	375	2 I38879	corticotropin rele
5	1550.5	65.1	411	2 A55810	corticotropin-rele
6	1543	64.8	431	2 I49149	CRF receptor - mou
7	1540.5	64.7	430	2 A56726	corticoliberin rec
8	1518.5	63.8	431	2 I49279	sauvagine/corticot
9	565	23.7	585	2 A39286	parathyroid hormon
10	554.5	23.3	593	2 A49191	parathyroid hormon
11	543.5	22.8	591	2 S44203	parathyroid hormon
12	543.5	22.8	591	2 I54195	parathyroid hormon
13	535	22.5	459	2 JH0594	vasoactive intesti
14	533	22.4	498	2 I47130	calcitonin recepto
15	531.5	22.3	449	2 I16319	secretin receptor
16	530	22.3	515	2 I49154	calcitonin recepto
17	527.5	22.2	589	2 I59297	parathyroid hormon
18	524	22.0	482	2 A39285	calcitonin recepto
19	518	21.8	440	2 JC2532	secretin receptor
20	518	21.8	495	2 JC2195	vasoactive intesti
21	513	21.5	490	2 S34486	calcitonin recepto
22	512.5	21.5	515	2 I60800	calcitonin recepto
23	511.5	21.5	479	2 S33746	calcitonin recepto
24	511	21.5	460	2 JC2194	vasoactive intesti
25	510.5	21.4	477	2 JC2041	glucagon recepto
26	510	21.4	474	2 I37217	calcitonin recepto
27	507	21.3	478	2 A37430	calcitonin recepto
28	504.5	21.2	550	2 A57519	parathyroid hormon
29	485.5	20.4	463	2 A46172	glucagon-like pept

30	485.5	20.4	485	2 JQ1957	glucagon receptor
31	483.5	20.3	485	2 JC4363	glucagon receptor
32	478	20.1	463	2 S71624	glucagon-like pept
33	477.5	20.1	464	2 I60194	calcitonin-like re
34	473.5	19.9	461	2 JC2477	calcitonin recepto
35	471.5	19.8	525	2 JN0902	pituitary adenylat
36	468.5	19.7	467	2 JN0616	pituitary adenylat
37	464	19.5	463	2 I84494	glucagon-like pept
38	459.5	19.3	438	2 G02822	vasoactive intesti
39	458.5	19.3	513	2 S47631	pituitary adenylat
40	455	19.1	451	2 I46586	growth hormone-rel
41	451.5	19.0	466	2 S66676	glucose-dependent
42	450.5	18.9	423	2 A45363	somatoliberin rece
43	450.5	18.9	495	2 S36114	pituitary adenylat
44	448.5	18.8	495	2 S39061	pituitary adenylat
45	448	18.8	466	2 G02234	gastric inhibitory

ALIGNMENTS

RESULT 1

A48260  
corticoliberin receptor, long splice form - human  
N;Alternate names: corticoliberin binding protein; corticotropin releasing factor recept  
C;Species: Homo sapiens (man)  
C;Date: 31-May-1996 #sequence revision 11-Apr-1997 #text\_change 09-Jul-2004  
C;Accession: I60975; A48260; S39534  
R;Chen, R.; Lewis, K.A.; Perrin, M.H.; Vale, W.W.  
Proc. Natl. Acad. Sci. U.S.A. 90, 8967-8971, 1993  
A;Title: Expression Cloning of a human corticotropin-releasing factor (CRF) receptor.  
A;Reference number: A48260; MUID:94022296; PMID:7692441  
A;Accession: I60975  
A;Status: translated from GB/EMBL/DDBJ  
A;Molecule type: mRNA  
A;Residues: 1-444 <RES>  
A;Cross-references: UNIPROT:P34998; UNIPARC:UPI0000128429; GB:L23333; NID:9408691; PIDN:?  
A;Experimental source: Cushing corticotropic cell tumor  
A;Accession: A48260  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A;Molecule type: mRNA  
A;Residues: 1-145,175-444 <RE2>  
A;Cross-references: UNIPARC:UPI000002A71D; GB:L23332; NID:9408689; PIDN:AAA35718.1; PID:?  
R;Vita, N.; Laurent, P.; Lefort, S.; Chalon, P.; Lelias, J.M.; Kaghad, M.; le Fur, G.; C  
FEBS Lett. 335, 1-5, 1993  
A;Title: Primary structure and functional expression of mouse pituitary and human brain c

A;Reference number: S39534; MUID:94063063; PMID:8243652  
A;Accession: S39534  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-145,175-444 <VIT>  
A;Cross-references: UNIPARC:UPI000002A71D; EMBL:X72304; NID:9436118; PIDN:CAA51052.1; PFI  
A;Note: the sequence from Fig. 1 is inconsistent with that from Fig. 3 in having an addit  
C;Genetics:  
A;Gene: GDB:CHRI; CHR: CRP-R; CRP1  
A;Cross-references: GDB:235922; OMIM:122561  
A;Map position: 17q12-17q22  
C;Superfamily: glucagon receptor  
C;Keywords: alternative splicing; transmembrane protein

Query Match	100.0%;	Score 2381;	DB 2;	Length 444;
Best Local Similarity	100.0%;	Pred. No. 4.6e-199;		
Matches 444;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0
Qy	1	MGHPQLRLVKALLLLGLNPVSASLODQHCEISLASNISGLQCNASVDLIGTCWPRSPA	60	
Db	1	MGHPQLRLVKALLLLGLNPVSASLODQHCEISLASNISGLQCNASVDLIGTCWPRSPA	60	
Qy	61	GLVVRPCPAFFYGVRYNTTNNNGRECLANGSWAARVNYSECQIILNEEKSKVHYHAV	120	
Db	61	GLVVRPCPAFFYGVRYNTTNNNGRECLANGSWAARVNYSECQIILNEEKSKVHYHAV	120	
Qy	121	IINYLGHCSLVALLVAVFLRLRPGCTHWGDAQDALEVPWGPQVPRRSICLR	180	

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Db 121 IINLGHGISLVALLVAFVFLRLRPGCTHWGQADGALVGPWMSGAPPQVRSIRCLR 160
QY 181 NIIHWNLSAFILRNATFVQVLTMSPEVHQSNVGCRLVTAAYNFHVTNPFWMFGECC 240
Db 181 NIIHWNLSAFILRNATFVQVLTMSPEVHQSNVGCRLVTAAYNFHVTNPFWMFGECC 240
QY 241 YLHTAIVLTYSTDRLRKMFVCIIGWGPVPIIIVAMAIGKLYYDNEKWCWPKRPGVYTDYI 300
Db 241 YLHTAIVLTYSTDRLRKMFVCIIGWGPVPIIIVAMAIGKLYYDNEKWCWPKRPGVYTDYI 300
QY 301 YQGPMLVLLINFIPLFNIVRIILMTKLRASTTSETIQYRKAVKATLVLLPLLGITTYMLFF 360
Db 301 YQGPMLVLLINFIPLFNIVRIILMTKLRASTTSETIQYRKAVKATLVLLPLLGITTYMLFF 360
QY 361 VNPGEDEVSRVVIYFNSFLESFGQFPVSVFYCFNLSEVRSAIRKRWHRWQDKHSIRARV 420
Db 361 VNPGEDEVSRVVIYFNSFLESFGQFPVSVFYCFNLSEVRSAIRKRWHRWQDKHSIRARV 420
QY 421 ARAMSIPTSPTRVSPHSIKQSTAV 444
Db 421 ARAMSIPTSPTRVSPHSIKQSTAV 444

RESULT 2
S39535
C:Species: Mus musculus (house mouse)
C:Date: 07-Oct-1994 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C:Accession: S39535
R;Vita, N.; Laurent, P.; Lefort, S.; Chalon, P.; Lelias, J.M.; le Fur, G.; C
PEBS Lett. 335, 1-5, 1993
A;Title: Primary structure and functional expression of mouse pituitary and human brain
A;Reference number: S39534; MUID:94063063; PMID:8243652
A;Accession: S39535
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-415 <VIT>
A;Cross-references: UNIPROT:P35347; UNIPARC:UPI0000027DE5; EMBL:X72305; NID:g436120; PID
A;Note: the sequence from Fig. 1 is inconsistent with that from Fig. 3 in having an addi
C;Superfamily: Glucagon receptor
C;Keywords: G protein-coupled receptor; transmembrane protein

Query Match 89.8%; Score 2137.5; DB 2; Length 415;
Best Local Similarity 91.2%; Pred. No. 6.2e-178; Mismatches 4; Indels 29; Gaps 1;
Matches 405; Conservative 4; Mismatches 6; Indels 29; Gaps 1;

QY 1 MGGHPQLRLVKALLLGLNPNVSASLQDQCHCESLSLASNISGLQCNASVDLIGTCWPRSPA 60
Db 1 MGQRPQLRLVKALLLGLNPNVSTLQDQCHCESLSLASNISGLQCNASVDLIGTCWPRSPA 60
QY 61 GQLVVRPCPAFFYGVRYNTNNGYRECLANGSWAARVNYSECQEIINEEKSKSVHYHVAV 120
Db 61 GQLVVRPCPAFFYGVRYNTNNGYRECLANGSWAARVNYSECQEIINEEKSKSVHYHVAV 120
QY 121 IINLGHGISLVALLVAFVFLRLRPGCTHWGQADGALVGPWMSGAPPQVRSIRCLR 180
Db 121 IINLGHGISLVALLVAFVFLRLRPGCTHWGQADGALVGPWMSGAPPQVRSIRCLR 180
QY 181 NIIHWNLSAFILRNATFVQVLTMSPEVHQSNVGCRLVTAAYNFHVTNPFWMFGECC 240
Db 181 NIIHWNLSAFILRNATFVQVLTMSPEVHQSNVGCRLVTAAYNFHVTNPFWMFGECC 240
QY 241 YLHTAIVLTYSTDRLRKMFVCIIGWGPVPIIIVAMAIGKLYYDNEKWCWPKRPGVYTDYI 300
Db 241 YLHTAIVLTYSTDRLRKMFVCIIGWGPVPIIIVAMAIGKLYYDNEKWCWPKRPGVYTDYI 300
QY 301 YQGPMLVLLINFIPLFNIVRIILMTKLRASTTSETIQYRKAVKATLVLLPLLGITTYMLFF 360
Db 301 YQGPMLVLLINFIPLFNIVRIILMTKLRASTTSETIQYRKAVKATLVLLPLLGITTYMLFF 360
QY 361 VNPGEDEVSRVVIYFNSFLESFGQFPVSVFYCFNLSEVRSAIRKRWHRWQDKHSIRARV 420
Db 361 VNPGEDEVSRVVIYFNSFLESFGQFPVSVFYCFNLSEVRSAIRKRWHRWQDKHSIRARV 420

RESULT 3
I58144
C:Species: Rattus norvegicus (Norway rat)
C:Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
C:Accession: I58144
R;Chang, C.P.; Pearce, R.V.; O'Connell, S.; Rosenfeld, M.G.
Neuron 11, 1187-1195, 1993
A;Title: Identification of a seven transmembrane helix receptor for corticotropin-releas
A;Reference number: I58144; MUID:94099969; PMID:8274282
A;Accession: I58144
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-415 <RES>
A;Cross-references: UNIPROT:P35353; UNIPARC:UPI000002EF2A; GB:L25438; NID:g450298; PID:n
C;Superfamily: Glucagon receptor

Query Match 89.3%; Score 2126.5; DB 2; Length 415;
Best Local Similarity 90.8%; Pred. No. 5.6e-177; Mismatches 5; Mismatches 7; Indels 29; Gaps 1;
Matches 403; Conservative 5; Mismatches 7; Indels 29; Gaps 1;

QY 1 MGGHPQLRLVKALLLGLNPNVSASLQDQCHCESLSLASNISGLQCNASVDLIGTCWPRSPA 60
Db 1 MGRRPQLRLVKALLLGLNPNVSTLQDQCHCESLSLASNISGLQCNASVDLIGTCWPRSPA 60
QY 61 GQLVVRPCPAFFYGVRYNTNNGYRECLANGSWAARVNYSECQEIINEEKSKSVHYHVAV 120
Db 61 GQLVVRPCPAFFYGVRYNTNNGYRECLANGSWAARVNYSECQEIINEEKSKSVHYHVAV 120
QY 121 IINLGHGISLVALLVAFVFLRLRPGCTHWGQADGALVGPWMSGAPPQVRSIRCLR 180
Db 121 IINLGHGISLVALLVAFVFLRLRPGCTHWGQADGALVGPWMSGAPPQVRSIRCLR 180
QY 181 NIIHWNLSAFILRNATFVQVLTMSPEVHQSNVGCRLVTAAYNFHVTNPFWMFGECC 240
Db 181 NIIHWNLSAFILRNATFVQVLTMSPEVHQSNVGCRLVTAAYNFHVTNPFWMFGECC 240
QY 241 YLHTAIVLTYSTDRLRKMFVCIIGWGPVPIIIVAMAIGKLYYDNEKWCWPKRPGVYTDYI 300
Db 241 YLHTAIVLTYSTDRLRKMFVCIIGWGPVPIIIVAMAIGKLYYDNEKWCWPKRPGVYTDYI 300
QY 301 YQGPMLVLLINFIPLFNIVRIILMTKLRASTTSETIQYRKAVKATLVLLPLLGITTYMLFF 360
Db 301 YQGPMLVLLINFIPLFNIVRIILMTKLRASTTSETIQYRKAVKATLVLLPLLGITTYMLFF 360
QY 361 VNPGEDEVSRVVIYFNSFLESFGQFPVSVFYCFNLSEVRSAIRKRWHRWQDKHSIRARV 420
Db 361 VNPGEDEVSRVVIYFNSFLESFGQFPVSVFYCFNLSEVRSAIRKRWHRWQDKHSIRARV 420
QY 421 ARAMSIPTSPTRVSPHSIKQSTAV 444
Db 421 ARAMSIPTSPTRVSPHSIKQSTAV 444

RESULT 4
I38879
C:Species: Homo sapiens (man)
C:Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004
C:Accession: I38879
R;Rosa, P.C.; Koets, C.M.; Ramabhadran, T.V.
Biochem. Biophys. Res. Commun. 205, 1836-1842, 1994
A;Title: A variant of the human corticotropin-releasing factor (CRF) receptor: cloning, e
A;Reference number: I38879; MUID:95110332; PMID:7811272
A;Accession: I38879
A;Status: preliminary; translated from GB/EMBL/DBJ
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Db 332 VNPGEDEVSRVVIYFNSFLESFGQFPVSVFYCFNLSEVRSAIRKRWHRWQDKHSIRARV 391
QY 421 ARAMSIPTSPTRVSPHSIKQSTAV 444
Db 392 ARAMSIPTSPTRVSPHSIKQSTAV 415

RESULT 3
I58144
C:Species: Rattus norvegicus (Norway rat)
C:Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
C:Accession: I58144
R;Chang, C.P.; Pearce, R.V.; O'Connell, S.; Rosenfeld, M.G.
Neuron 11, 1187-1195, 1993
A;Title: Identification of a seven transmembrane helix receptor for corticotropin-releas
A;Reference number: I58144; MUID:94099969; PMID:8274282
A;Accession: I58144
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-415 <RES>
A;Cross-references: UNIPROT:P35353; UNIPARC:UPI000002EF2A; GB:L25438; NID:g450298; PID:n
C;Superfamily: Glucagon receptor

Query Match 89.3%; Score 2126.5; DB 2; Length 415;
Best Local Similarity 90.8%; Pred. No. 5.6e-177; Mismatches 5; Mismatches 7; Indels 29; Gaps 1;
Matches 403; Conservative 5; Mismatches 7; Indels 29; Gaps 1;

QY 1 MGGHPQLRLVKALLLGLNPNVSASLQDQCHCESLSLASNISGLQCNASVDLIGTCWPRSPA 60
Db 1 MGRRPQLRLVKALLLGLNPNVSTLQDQCHCESLSLASNISGLQCNASVDLIGTCWPRSPA 60
QY 61 GQLVVRPCPAFFYGVRYNTNNGYRECLANGSWAARVNYSECQEIINEEKSKSVHYHVAV 120
Db 61 GQLVVRPCPAFFYGVRYNTNNGYRECLANGSWAARVNYSECQEIINEEKSKSVHYHVAV 120
QY 121 IINLGHGISLVALLVAFVFLRLRPGCTHWGQADGALVGPWMSGAPPQVRSIRCLR 180
Db 121 IINLGHGISLVALLVAFVFLRLRPGCTHWGQADGALVGPWMSGAPPQVRSIRCLR 180
QY 181 NIIHWNLSAFILRNATFVQVLTMSPEVHQSNVGCRLVTAAYNFHVTNPFWMFGECC 240
Db 181 NIIHWNLSAFILRNATFVQVLTMSPEVHQSNVGCRLVTAAYNFHVTNPFWMFGECC 240
QY 241 YLHTAIVLTYSTDRLRKMFVCIIGWGPVPIIIVAMAIGKLYYDNEKWCWPKRPGVYTDYI 300
Db 241 YLHTAIVLTYSTDRLRKMFVCIIGWGPVPIIIVAMAIGKLYYDNEKWCWPKRPGVYTDYI 300
QY 301 YQGPMLVLLINFIPLFNIVRIILMTKLRASTTSETIQYRKAVKATLVLLPLLGITTYMLFF 360
Db 301 YQGPMLVLLINFIPLFNIVRIILMTKLRASTTSETIQYRKAVKATLVLLPLLGITTYMLFF 360
QY 361 VNPGEDEVSRVVIYFNSFLESFGQFPVSVFYCFNLSEVRSAIRKRWHRWQDKHSIRARV 420
Db 361 VNPGEDEVSRVVIYFNSFLESFGQFPVSVFYCFNLSEVRSAIRKRWHRWQDKHSIRARV 420
QY 421 ARAMSIPTSPTRVSPHSIKQSTAV 444
Db 421 ARAMSIPTSPTRVSPHSIKQSTAV 415

RESULT 4
I38879
C:Species: Homo sapiens (man)
C:Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004
C:Accession: I38879
R;Rosa, P.C.; Koets, C.M.; Ramabhadran, T.V.
Biochem. Biophys. Res. Commun. 205, 1836-1842, 1994
A;Title: A variant of the human corticotropin-releasing factor (CRF) receptor: cloning, e
A;Reference number: I38879; MUID:95110332; PMID:7811272
A;Accession: I38879
A;Status: preliminary; translated from GB/EMBL/DBJ
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A:Molecule type: mRNA  
A:Residues: 1-375 <RES>  
A:Cross-references: UNIPROT:P34998; UNIPARC:UPI000002A71B; EMBL:U16273; NID:9606973; PII  
C:Superfamily: glucagon receptor

Query Match 80.9%; Score 1925.5; DB 2; Length 375;  
Best Local Similarity 84.2%; Pred. No. 1.5e-159;  
Matches 374; Conservative 1; Mismatches 0; Indels 69; Gaps 2;

QY 1 MGGHPQLRLVKALLLGLNPVSASLODQHCHESISLASNISGLQCNASVDLIGTCWPRSPA 60  
DB 1 MGGHPQLRLVKALLLGLNPVSASLODQHCHESISLASNIS----- 40

QY 61 GQLVVRPCPAFFYGVRYNTNNGYRECLANGSWAARVNSCOEILNEEKSKVHHVAV 120  
DB 41 -----DNGYRECLANGSWAARVNSCOEILNEEKSKVHHVAV 80

QY 121 IINYLGHCSISLVALVAFVFLRLRPGCTHWGQADGALVGVAPWSGAPQVRRSIRCLR 180  
DB 81 IINYLGHCSISLVALVAFVFLRL-----RSIRCLR 111

QY 181 NIIHWNLSAFILRNATFVQVLTMSPEVHQSNGVWCRLVTAAYNFVHTNPFWMFEGGC 240  
DB 112 NIIHWNLSAFILRNATFVQVLTMSPEVHQSNGVWCRLVTAAYNFVHTNPFWMFEGGC 171

QY 241 YLHTAIVLTSTDRLRKRMFICIGWGVPPIIIVAWAIGKUYDNEKWCWFKRPGVTDYI 300  
DB 172 YLHTAIVLTSTDRLRKRMFICIGWGVPPIIIVAWAIGKUYDNEKWCWFKRPGVTDYI 231

QY 301 YQGPMLVLLINFIPLFNIRIILMTKLRASTTSETIOYRKAVKATVLLPLLGITMYLFF 360  
DB 232 YQGPMLVLLINFIPLFNIRIILMTKLRASTTSETIOYRKAVKATVLLPLLGITMYLFF 291

QY 361 VNPGEDEVSRVFIYFNSFLESQGFVSVFYCFNLSEVRSALRKRWHRQDQKHSIRARV 420  
DB 292 VNPGEDEVSRVFIYFNSFLESQGFVSVFYCFNLSEVRSALRKRWHRQDQKHSIRARV 351

QY 421 ARAMSIPSTRVSVFHSIKOSTAV 444  
DB 352 ARAMSIPSTRVSVFHSIKOSTAV 375

RESULT 5  
A55610  
corticotropin-releasing factor receptor subtype 2 - rat  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 09-Jul-2004  
C:Accession: A55610  
R;Jovenberg, T.W.; Liaw, C.W.; Grigoriadis, D.B.; Clevenger, W.; Chalmers, D.T.; De Souza  
Proc. Natl. Acad. Sci. U.S.A. 92, 836-840, 1995  
A;Title: Cloning and characterization of a functionally distinct corticotropin-releasing  
A;Reference number: A55610; MUID:95148632; PMID:7846062  
A;Accession: A55610  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-411 <LOV>  
A:Cross-references: UNIPROT:P47866; UNIPARC:UPI000012842E; EMBL:U16253; NID:9644771; PII  
C:Genetics:  
A:Gene: CRF2R  
C:Superfamily: glucagon receptor

Query Match 65.1%; Score 1550.5; DB 2; Length 411;  
Best Local Similarity 64.9%; Pred. No. 6.3e-127;  
Matches 290; Conservative 59; Mismatches 52; Indels 53; Gaps 6;

QY 12 ALLLGLNPVSASLODQHCHESISLASNI-----SGLQCNASVDLIGTCWPRS 58  
DB 4 ALLL-----SLLEANC-SLALABELLDGGEPPDPGPGSYNCNTTLDQIGTCWPQS 54

QY 59 PAGQLVVRPCPAFFYGVRYNTNNGYRECLANGSWAARVNSCOEILNE-EKSKVHHV 117  
DB 55 APGALVERPCPFYNGIKYNTTRNAYRECLANGSWAARVNSHCEPILDDKQRKYDLYR 114

QY 118 VAVIINYLGHCSISLVALVAFVFLRLRPGCTHWGQADGALVGVAPWSGAPQVRRSIR 177  
DB 115 IALIINYLGHCSVVALVAAFLFL-----VLRSSIR 145

QY 178 CLRNIIHWNLSAFILRNATFVQVLTMSPEVHQSNGVWCRLVTAAYNFVHTNPFWMF 237  
DB 146 CLRNIIHWNLSAFILRNATFVQVLTMSPEVHQSNGVWCRLVTAAYNFVHTNPFWMF 204

QY 238 EGYLHTAIVLTSTDRLRKRMFICIGWGVPPIIIVAWAIGKUYDNEKWCWFKRPGVYT 297  
DB 205 EGYLHTAIVLTSTDRLRKRMFICIGWGVPPIIIVAWAIGKUYDNEKWCWFKRPGVYT 264

QY 298 DYIQGPMLVLLINFIPLFNIRIILMTKLRASTTSETIOYRKAVKATVLLPLLGITMY 357  
DB 265 DYIQGPMLVLLINFIPLFNIRIILMTKLRASTTSETIOYRKAVKATVLLPLLGITMY 324

QY 358 LFFVNPGEDEVSRVFIYFNSFLESQGFVSVFYCFNLSEVRSALRKRWHRQDQKHSIR 417  
DB 325 LFFVNPGEDEVSRVFIYFNSFLESQGFVSVFYCFNLSEVRSALRKRWHRQDQKHSIR 384

QY 418 ARVARAMSIPSTRVSVFHSIKOSTAV 444  
DB 385 VPVARAMSIPSTRVSVFHSIKOSTAV 411

RESULT 6  
I49149  
CRF receptor - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 09-Jul-2004  
C:Accession: I49149  
R;Ferrin, M.; Donaldson, C.; Chen, R.; Blount, A.; Berggren, T.; Bilezikjian, L.; Sawcher  
Proc. Natl. Acad. Sci. U.S.A. 92, 2969-2973, 1995  
A;Title: Identification of a second corticotropin-releasing factor receptor gene and char  
A;Reference number: I49149; MUID:95224061; PMID:7708757  
A;Accession: I49149  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-431 <RES>  
A:Cross-references: UNIPROT:Q60748; UNIPARC:UPI0000028473; EMBL:U17858; NID:9727254; PII  
C:Superfamily: glucagon receptor

Query Match 64.8%; Score 1543; DB 2; Length 431;  
Best Local Similarity 62.4%; Pred. No. 3e-126;  
Matches 287; Conservative 59; Mismatches 64; Indels 50; Gaps 7;

QY 2 GHPQLRLVKALLLGLNPVSA-----SLODQHCHESISLASNISG--LQCN 45  
DB 5 GSLPSAQLL--LCLFSLPLVQVQAQAPQDQPLMTLLEQYCHRTTI-GNFSGPYYTCN 61

QY 46 ASVDLIGTCWPRSPAGQLVVRPCPAFFYGVRYNTNNGYRECLANGSWAARVNSCOEI 105  
DB 62 TTLDQIGTCWPQSAPGALVERPCPFYNGIKYNTTRNAYRECLANGSWAARVNSHCEPI 121

QY 106 LNE-EKSKVHHVAVIINYLGHCSISLVALVAFVFLRLRPGCTHWGQADGALVGVAP 164  
DB 122 LDDKQRKYDLYRIALIINYLGHCSVVALVAAFLFL----- 159

QY 165 WSGAPQVRRSIRCLRNIHWNLSAFILRNATFVQVLTMSPEVHQSNGVWCRLVTAAY 224  
DB 160 -----VLRSSIRCLRNIHWNLSAFILRNATFVQVLTMSPEVHQSNGVWCRLVTAAY 211

QY 225 NYFHTNPFWMFEGGCYLHTAIVLTSTDRLRKRMFICIGWGVPPIIIVAWAIGKUYD 284  
DB 212 NYFHTNPFWMFEGGCYLHTAIVLTSTDRLRKRMFICIGWGVPPIIIVAWAIGKUYD 271

QY 285 EKCFWFKRPGVTDYIYQGPMLVLLINFIPLFNIRIILMTKLRASTTSETIOYRKAVKA 344  
DB 272 EKCFWFKRPGVTDYIYQGPMLVLLINFIPLFNIRIILMTKLRASTTSETIOYRKAVKA 331

QY 345 TLVLLPLLGITMYLFFVNPGEDEVSRVFIYFNSFLESQGFVSVFYCFNLSEVRSIR 404  
DB 332 TLVLLPLLGITMYLFFVNPGEDEVSRVFIYFNSFLESQGFVSVFYCFNLSEVRSIR 391



Db 204 LI-----LGYFRLHCTRNYYIHHHLFVSPMLRAVSI 234  
QY 199 FVYQ-----LTMSPEVHQSNVGVKRLVTAAYNYFHVTFNPFWMF 236  
Db 235 FIKDAVLYSGVSTDEITERITEBELRAFTPEPPADKAGFCVCRVAVTVFLYFLTTNYWIL 294  
QY 237 GEGCYLHTAIVLYSTDRLRKWMFICIGWGVPPPIIVAWAIGKLYDYNEKCM---FGKRP 293  
Db 295 VEGLYLHSLIFMAFFSEKKYLMGFTLFGWGLPAVFVAVVTVVRATLANTECDLSSGNK- 353  
QY 294 GVTVDIYOGPMILVLLINFIPLFNIRIILMTKLR---ASTTSETIQYRKAVKATLVLLP 350  
Db 354 ----KWLIIQVPIIALAVNVFIPLFNIRIILMTKLR---ASTTSETIQYRKAVKATLVLLP 409  
QY 351 LLGITVLMFVNPGEDEVSRVVF---IYFNSFLSFQGFVSVFYCFNLSEVSAIRKRW 407  
Db 410 LFGVHYIVFMAFP-YTEVSGILLQVQMHYEMFLNSFGFFVAIYFCNGEVAEIKKSW 468  
QY 408 HRW 410  
Db 469 SRW 471

RESULT 10  
A49191  
parathyroid hormone/PTH-related peptide receptor - human  
N/Alternate names: parathyroid hormone/parathyroid hormone related peptide receptor  
C/Species: Homo sapiens (man)  
C/Date: 19-Dec-1993 #sequence revision 18-Nov-1994 #text\_change 09-Jul-2004  
C/Accession: I38139; A49191; I38113; G01562; S29610  
R/Schipani, E.; Weinstein, L.S.; Bergwitz, C.; Iida-Klein, A.; Kong, X.F.; Stuhmann, M.  
Kronenberg, H.M.; Abou-Samra, A.B.; Segre, G.V.; Jueppner, H.  
J. Clin. Endocrinol. Metab. 80, 1611-1621, 1995  
A/Title: Pseudohypoparathyroidism type 1b is not caused by mutations in the coding exons  
A/Reference number: I38139; MUID:95263723; PMID:7745008  
A/Accession: I38139  
A/Status: translated from GB/EMBL/DBJ  
A/Molecule type: DNA  
A/Residues: 1-593 <RES>  
A/Cross-references: UNIPROT:Q03431; UNIPARC:UPI000005041F; EMBL:U22409; NID:g987594; PID:  
R/Schipani, E.; Karga, H.; Karaplis, A.C.; Potte Jr., J.T.; Kronenberg, H.M.; Segre, G.V.  
Endocrinology 132, 2157-2165, 1993  
A/Title: Identical complementary deoxyribonucleic acids encode a human renal and bone pa  
A/Reference number: A49191; MUID:93238641; PMID:8386612  
A/Accession: A49191  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-593 <SCH>  
A/Cross-references: UNIPARC:UPI000005041F; GB:I04308; NID:g190721; PIDN:AAA36525.1; PID:  
A/Note: sequence extracted from NCBI backbone (NCBIN:130233, NCBIP:130234)  
R/Schneider, H.; Feyen, J.H.; Seuwen, K.; Movva, N.R.  
Eur. J. Pharmacol. 246, 149-155, 1993  
A/Title: Cloning and functional expression of a human parathyroid hormone receptor.  
A/Reference number: I38113; MUID:93387403; PMID:8397094  
A/Accession: I38113  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: mRNA  
A/Residues: 1-593 <RE2>  
A/Cross-references: UNIPARC:UPI000005041F; EMBL:X68596; NID:g396812; PIDN:CAA48589.1; PI  
R/Levine, M.  
submitted to the EMBL Data Library, November 1994  
A/Reference number: G07787  
A/Accession: G01562  
A/Status: translated from GB/EMBL/DBJ  
A/Molecule type: mRNA  
A/Residues: 1-593 <LEV>  
A/Cross-references: UNIPARC:UPI000005041F; EMBL:U17418; NID:g596129; PIDN:AAA56774.1; PI  
C/Genetics:  
A/Introns: 25/3; 60/1; 105/1; 142/1; 181/3; 213/2; 278/3; 330/1; 350/2; 372/3; 404/2; 45  
C/Superfamily: glucagon receptor  
C/Keywords: G protein-coupled receptor; transmembrane protein

Query Match 23.3%; Score 554.5; DB 2; Length 593;  
Best Local Similarity 31.6%; Pred. No. 3.4e-40;  
Matches 131; Conservative 58; Mismatches 147; Indels 79; Gaps 12;  
QY 37 SNISGLQCNASVDLIGTCWPRSPAGQVVRPCPAFFYGVRYNTTNGYRECLANGSW--- 93  
Db 101 SYRGRPCLPWDHI-LCWPLGAPGBVAVPCPDYID--FNHKGHYRRCDRNGSWELV 157  
QY 94 ----AARVNYSCOEILNEBKSKVHYHVAVIINYLGHCISLVALLVAVFLRLRPCT 149  
Db 158 PGHNRTWANYSECVKPLTNETREREVEFDRLGMIYTVGVSVSLASTVA-VLIL- 209  
QY 150 HNGDQADGALEVGAPWSPGAPFQVRRSIRCLRNIIHWNLISAFILRNATVFW- 200  
Db 210 -----AYF---RRLHCTRNYIHHMLFLSPMLRAVSI-FVKDAVLYSGA 248  
QY 201 -----VQLTMSPEVHQSNVGVKRLVTAAYNYFHVTFNPFWMFGECCYLHT 244  
Db 249 TLDEAERLTTEBELRAIAQAAPPPTATAAGVAGCRVAVTFPLFLATNYYWILVEGLYLS 308  
QY 245 AIVLYSTDRLRKWMFICIGWGVPPPIIVAWAIGKLYDYNEKCM---FGKRPVYTDYIY 301  
Db 309 LIFMAFFSEKKYLMGFTVFGWGLPAVFVAVVTVVRATLANTECDLSSGNK----KWLII 363  
QY 302 QGPMILVLLINFIPLFNIRIILMTKLR---ASTTSETIQYRKAVKATLVLLPILGITYML 358  
Db 364 QVPIIASIVNFIPLFNIRIILMTKLR---ASTTSETIQYRKAVKATLVLLPILGITYML 423  
QY 359 FFVNPGEDEVSRVVF---IYFNSFLSFQGFVSVFYCFNLSEVSAIRKRW 410  
Db 424 FMAFP-YTEVSGILLQVQMHYEMFLNSFGFFVAIYFCNGEVAEIKKSW 477

RESULT 11  
S44203  
parathyroid hormone-related peptide receptor - mouse  
C/Species: Mus musculus (house mouse)  
C/Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 09-Jul-2004  
C/Accession: S44203  
R/Karperien, M.; van Dijk, T.B.; Hoeijmakers, T.; Cremers, F.; Abou-Samra, A.B.; Boonstra  
submitted to the EMBL Data Library, April 1994  
A/Description: Expression pattern of parathyroid hormone/parathyroid hormone related pept  
A/Reference number: S44203  
A/Accession: S44203  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-591 <KAR>  
A/Cross-references: UNIPROT:P41593; UNIPARC:UPI0000027984; EMBL:X78936; NID:g474828; PIDN  
C/Superfamily: glucagon receptor

Query Match 22.8%; Score 543.5; DB 2; Length 591;  
Best Local Similarity 31.6%; Pred. No. 3e-39;  
Matches 129; Conservative 63; Mismatches 143; Indels 73; Gaps 13;  
QY 41 GLOCNASVDLIGTCWPRSPAGQVVRPCPAFFYGVRYNTTNGYRECLANGSW----- 93  
Db 105 GRPCLPEWDNI-VCWPLGAPGBVAVPCPDYID--FNHKGHYRRCDRNGSWVPGHN 161  
QY 94 AARVNYSCOEILNEBKSKVHYHVAVIINYLGHCISLVALLVAVFLRLRPCTHMGD 153  
Db 162 RTWANYSECLKFWNETREREVEFDRLGMIYTVGVSVSLASTVA-VLIL- 209  
QY 154 QADGALEVGAPWSPGAPFQVRRSIRCLRNIIHWNLISAFILRNATVFWVQLTM----- 205  
Db 210 -----AYF---RRLHCTRNYIHHMLFLSPMLRAVSI-FVKDAVLYSGFTLDE 252  
QY 206 -----SPEVH-----QSNVGV---CRLVTAAYNYFHVTFNPFWMFGECCYLHTAIVL 248  
Db 253 AERLTTEBELHIIAQVPPPPAAAAGVAGCRVAVTFPLFLATNYYWILVEGLYLSIFM 312  
QY 249 TYSTDRLRKWMFICIGWGVPPPIIVAWAIGKLYDYNEKCMFGKRPVYTDYIYQGPMILV 308  
Db 313 AFFSEKKYLMGFTVFGWGLPAVFVAVVTVVRATLANTECDLSSGNK----KWLIIQVPIIL 370

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QY 309 LLINFIPLFNIVRLMTKLR---ASTTSETIQYRKAVKATLVLLPLLGITYMLFFVNPGE 365
Db 371 VLVNFIPLFINIIRVATKLRRTNAGRCDDTRQYRKLLRSTLVLPVLFVGHVYTVFMALP-Y 429
QY 366 DEYSRVVVF---IYFNSFLESFQGFVSVFYCFNLSEVRSRAIRKRW 410
Db 430 TEVSGTLWQIQMHYEMLFNSFQGFVVAIIYFCNGEVAEIRKSWGRW 477

RESULT 12
I54195
parathyroid hormone/parathyroid hormone related-peptide receptor - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 09-Jul-2004
C/Accession: I54195; A42698
R/Pausova, Z.; Bourdon, J.; Clayton, D.; Mattei, M.G.; Seldin, M.F.; Janicic, N.; Rivier
Genomics 20, 20-26, 1994
A/Title: Cloning of a parathyroid hormone/parathyroid hormone-related peptide receptor
and rat genomes.
A/Reference number: I54195; MUID:94292182; PMID:8020952
A/Accession: I54195
A/Status: preliminary; translated from GB/EMBL/DDBJ
A/Molecule type: mRNA
A/Residues: 1-591 <RES>
A/Cross-references: UNIPROT:P25961; UNIPARC:UPI00001329C2; GB:L19475; NID:G4673116; PIDN:
R/Abou-Samra, A.B.; Juppner, H.; Force, T.; Freeman, M.W.; Kong, X.F.; Schipani, E.; Ure
Proc. Natl. Acad. Sci. U.S.A. 89, 2732-2736, 1992
A/Title: Expression cloning of a common receptor for parathyroid hormone and parathyroid
n of both CAMP and inositol trisphosphates and increases intracellular free calcium.
A/Reference number: A42698; MUID:92212903; PMID:1313566
A/Accession: A42698
A/Status: preliminary; not compared with conceptual translation
A/Molecule type: DNA
A/Residues: 1-585, 'G', 587-591 <ABO>
A/Cross-references: UNIPARC:UPI00001789A7
A/Experimental source: ROS 17/2.8 osteosarcoma cells
A/Note: sequence extracted from NCBI backbone (NCBIP:92187)
C/Superfamily: glucagon receptor

Query Match 22.8%; Score 543.5; DB 2; Length 591;
Best Local Similarity 31.6%; Pred. No. 3e-39;
Matches 129; Conservative 63; Mismatches 143; Indels 73; Gaps 13;

QY 41 GLOCNASVDLIGTCWPSRPAQGLVVRPCPAFFGVRYNTNNGYRECLANGSW----- 93
Db 105 GRPCLPEWDNI-VCMPLGAPGEVAVPCPDYID--FNHKGHAYRCDRNGSEVVPGHN 161
QY 94 AARVNYSECOEILNEEKKSVHYHVAIIVNLGHCTSLVALLVAVFLRLRPGCTHWGD 153
Db 162 RTWANYSECLKFTNTREREVEFDRLGMIVTVGYSMSLASLTVV-LVIL----- 209
QY 154 QADGALEVGAPSGAPQVRRSIRCLRNIIHWNLIISAFILRNATWVVLQTM----- 205
Db 210 -----AVP-----RLHCTRNYYIHMLFMSFLRAASIFVKDAVLYSGTFLDE 252
QY 206 -----SPEVH-----QSNVGV--CHLVTAANYFHVTFNFMFGECYLHAIVL 248
Db 253 AERLTEELHIIAQVPPPPAAAAGVAGCRVAVTFPLYPATNYYIWLVEGLYLHSLIPM 312
QY 249 TYGTDRLRKMMFICIGWGPFPPIIWAIGKLYVDNEKCFGRKPGVYTDYIYQGPMLIV 308
Db 313 AFPESEKKYLMGFTIFGWLPAFVAVWVGRATLANTGCV--DLSSGHKKWIIQVILAS 370
QY 309 LLINFIPLFNIVRLMTKLR---ASTTSETIQYRKAVKATLVLLPLLGITYMLFFVNPGE 365
Db 371 VLVNFIPLFINIIRVATKLRRTNAGRCDDTRQYRKLLRSTLVLPVLFVGHVYTVFMALP-Y 429
QY 366 DEYSRVVVF---IYFNSFLESFQGFVSVFYCFNLSEVRSRAIRKRW 410
Db 430 TEVSGTLWQIQMHYEMLFNSFQGFVVAIIYFCNGEVAEIRKSWGRW 477
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RESULT 13
JH0594
vasoactive intestinal peptide receptor precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 09-Jul-2004
C/Accession: JH0594; S56014
R/Tshihara, T.; Shigemoto, R.; Mori, K.; Takahashi, K.; Nagata, S.
Neuron 8, 811-819, 1992
A/Title: Functional expression and tissue distribution of a novel receptor for vasoactive
A/Reference number: JH0594; MUID:92232309; PMID:1314625
A/Accession: JH0594
A/Molecule type: mRNA
A/Residues: 1-459 <ISH>
A/Cross-references: UNIPROT:P30083; UNIPARC:UPI0000055A96; GB:M86835; NID:G207640; PIDN:
R/Pei, L.; Melmed, S.
Biochem. J. 308, 719-723, 1995
A/Title: Characterization of the rat vasoactive intestinal polypeptide receptor gene 5'
A/Reference number: S56014; MUID:97104266; PMID:8948424
A/Accession: S56014
A/Status: preliminary; translation not shown
A/Molecule type: DNA
A/Residues: 1-26 <PEI>
A/Cross-references: UNIPARC:UPI000000053A; EMBL:U10635; NID:G505752; PIDN:AA848185.1; PII
C/Superfamily: glucagon receptor
C/Keywords: G protein-coupled receptor; glycoprotein; intestine; transmembrane protein
F/1-30/Domain: signal sequence #status predicted <SIG>
F/31-459/Product: vasoactive intestinal polypeptide receptor #status predicted <MAT>
F/146-168/Domain: transmembrane #status predicted <TM1>
F/176-195/Domain: transmembrane #status predicted <TM2>
F/218-241/Domain: transmembrane #status predicted <TM3>
F/256-277/Domain: transmembrane #status predicted <TM4>
F/295-318/Domain: transmembrane #status predicted <TM5>
F/344-363/Domain: transmembrane #status predicted <TM6>
F/376-395/Domain: transmembrane #status predicted <TM7>
F/58,69,100,292/Binding site: carbohydrate (Asn) #status predicted

Query Match 22.5%; Score 535; DB 2; Length 459;
Best Local Similarity 29.5%; Pred. No. 1.2e-38;
Matches 132; Conservative 80; Mismatches 149; Indels 86; Gaps 17;

QY 5 POLR---LVKALLLGLNPFV-SASLDQDH-CBSLSIASNISGLQCNASVDLIG----- 52
Db 7 PHVRMLCVLAGALCALRPAGQAASPOHECVLQI-LIQRCQCLEBAQLNETTGTCSK 65
QY 53 -----TCWPRSPAGQLVVRPCPAFP-----YGVRYNTNNGYRECLANGSWAARVNY 99
Db 66 MWDNLTCWPTTPRQAVVLDCLIFQLFAPFIHGYNISRCTBEGWSQ-LEPGPYHIAAGL 124
QY 100 SECOETLNEEKKSVHYHVAIIVNLGHCTSLVALLVAVFLRLRPGCTHWGDQADGA 158
Db 125 NDRASLDEQQQTK--FYNTVKTGYTIGYSLASLLVAVAI----- 164
QY 159 LEVGAPWSGAPQVRRSIRCLRNIIHWNLIISAFILRNATWVVLQTM--SPEV---HQSN 213
Db 165 -----LSLFLKLTCHTRNYIHMLFMSFILRATAVFIKDMALFNSGEIDHCSEAS 213
QY 214 VMCRLVTAANYFHVTFNFMFGECYLHAIVLTYSTDRLRKMMFICIGWGPFPPIIV 273
Db 214 VG-CRAAVVFFQVCYMANPFWLLVEGLYLYTLTLLAVSFPSERKYFWGYYILIGWGPSVFT 272
QY 274 AWAIGKLYVDNEKCFGRKPGVYTD-----YIYQGPMLIVLLNPIFLFNIVRLMT 325
Db 273 ITWTVRIYDEFGCV-----DTIINSSLWIIKAPILSILVNFIFCIIILVQ 323
QY 326 KLRASV--TSETIQYRKAVKATLVLLPLLGITYMLFFVNPGEDEVSRVYFVNSFLESF 383
Db 324 KLRPPDIGKNDSSPSRLAKSTLLIPLFGIHYVMPAFP--DNFKAQKMWVPELVVGSF 381
QY 384 QGFVSVFYCFNLSEVRSRAIRKRW 410
Db 382 QGFVVAIYCFNLSEVRSRAIRKRW 408
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RESULT 14  
I47130  
calcitonin receptor-lb - pig  
C;Species: Sus scrofa domestica (domestic pig)  
C;Date: 21-Feb-1997 #sequence\_revision 21-Feb-1997 #text\_change 09-Jul-2004  
C;Accession: I47130  
R;Zolnierowicz, S.; Cron, P.; Solinas-Toldo, S.; Fries, R.; Lin, H.Y.; Hemmings, B.A.  
J. Biol. Chem. 269, 19530-19538, 1994  
A;Title: Isolation, characterization, and chromosomal localization of the porcine calcitonin receptor  
A;Reference number: A53972; MUID:94308241; PMID:8034723  
A;Accession: I47130  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-498 <20>  
A;Cross-references: UNIPROT:P25117; UNIPARC:UPI0000126E78; EMBL:Z31356; NID:9531126; PDB:1WVW  
C;Genetics:  
A;Introns: 17/3; 70/1; 107/1; 144/3; 175/2; 233/3; 285/1; 305/2; 327/3; 400/3; 414/3  
C;Superfamily: glucagon receptor  
  
Query Match 22.4%; Score 533; DB 2; Length 498;  
Best Local Similarity 32.0%; Pred. No. 2e-38;  
Matches 129; Conservative 84; Mismatches 142; Indels 48; Gaps 15;  
  
QY 41 GLOCNASVDLIG-TCHPRSPAGQIVRPPCPAPP--YGVRYNTT-----NNGYRECLANG 91  
DB 70 GLYCNRTWD--GWSWDDTDPAGVLAECYCPDPFDDAEKVKYKCGEDGDWYRHPSNI 127  
QY 92 SWAARNYSECQELNEE-KKSKVHVHVAIIVNLYGHICISLVALVAFVFLRLRPGCTH 150  
DB 128 SWS---NYTWCNAFTDKQNAVILYLAIV-----GHSLSITLLSLGIFMFLR 175  
QY 151 WGDQADGALEVGAPGAPQVRRSIRCLRNIIHWNLIISAFILRNATFWVVLQTM---SP 207  
DB 176 -----YFNLLAPFNALLYPT-RSISQVRVTLHKMFLTYVL-NSIIIVHLVWVTPNG 226  
QY 208 EVHQSNVGVCRLYTAANYPHVTNFFWFGEGCYLHTAIVLTYSTDLRKWMFICIGWGV 267  
DB 227 ELVKRDPPICKVLHFFHQYMMSCNYFMWLCGCVLYLTLIVVSVFAEQRLMWHYVLGWF 286  
QY 268 PPIIIVAWAIGKLYDNEKCFGRPGVYTD--YIYQGPMLVLLINFIENIVRILMT 325  
DB 287 PLIPTTAHATRAVLFDNDCWL-----SVDNLLYIIGHVPVMAALVNVFFLLNLRVLVK 342  
QY 326 KLRASSTSETIQYRKAVKATLVLLPLLGITYMLFFVNPGEDEVSRVVFYFNFSFLESFQ 385  
DB 343 KLKESQEAESHMYLKAVRATLILVPLLGQVFLVWPRSTPLLGK-IYDYVHSLIHFG 401  
QY 386 FFVSFVFCFLNSVRSAIRKRWH-----RWODKHSIRARVARA 423  
DB 402 FFVAIIYFCNHEVOGALKRQWQYQQRWAGRRSTRAANAAA 444  
  
RESULT 15  
S16319  
secretin receptor - rat  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 09-Jul-2004  
C;Accession: S16319  
R;Ishihara, T.; Nakamura, S.; Kaziro, Y.; Takahashi, T.; Takahashi, K.; Nagata, S.  
EMBO J. 10, 1635-1641, 1991  
A;Title: Molecular cloning and expression of a cDNA encoding the secretin receptor.  
A;Reference number: S16319; MUID:91266890; PMID:1646711  
A;Accession: S16319  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-449 <1SH>  
A;Cross-references: UNIPROT:P23811; UNIPARC:UPI000013569A; EMBL:X59132; NID:957228; PDB:1WVW  
C;Superfamily: glucagon receptor  
C;Keywords: G protein-coupled receptor; transmembrane protein  
  
Query Match 22.3%; Score 531.5; DB 2; Length 449;  
Best Local Similarity 31.7%; Pred. No. 2.5e-38;

Matches 152; Conservative 64; Mismatches 154; Indels 109; Gaps 20;  
QY 7 LRLVKALLLLGNP-----VSASLQDQ--HC-BELS-----LASNISGLQCNASVD 49  
DB 17 LLLTKAAHTVGVPPRLCDVRRVLLERAHCLQOLSKEKKGALGPETASGCEGLWNNMS-- 74  
QY 50 LIGTCWPRSPAGQIVRPPCPAPPY-----GVRYNTTNGYRECLANGSWAARVNYSEC 102  
DB 75 -----CWPSAPARTVEQCCKPFLMLSNKNGSLFRNCTQDGWSETFPRPDLAGCVNINS 130  
QY 103 QEILNEEK-----KSKVHVHVAIIVNLYGHICISLVALVAFVFLRLRPGCTHMGDQADG 157  
DB 131 ---FNERRHAYLLKLKVMYTV-----GVSSSLAMLLVALSIL-----CSF----- 167  
QY 158 ALEVGAPWSGAPQVRRSIRCLRNIIHWNLIISAFILRNATFWV--VOLTMSPEV---HQS 212  
DB 168 -----RRLHCTRYNIHMLFVSVFILRALSNFIKDAVLFSSDDVTYCDAAH 211  
QY 213 NVGWCCLVTAANYPHVTNFFWFGEGCYLHTAIVLTYSTDLRKWMFICIGWGVPPPII 272  
DB 212 KVG-CKLVMIFFQYCIIMANYAMLLVEGLYLLTLAISFFSERKYLOAFVLLGWSGSPAIFV 270  
QY 273 VAWAIGKLYDNEKWC-FGKRPGVYTDYIYQGPMLVLLINFIENIVRILMTKLRAS 331  
DB 271 ALMAITRHFLENTGCGWDINANASVW--WIRGVPVILSILINFIENILRLMKLRTOE 328  
QY 332 T--SETIQYRKAVKATLVLLPLLGITYMLFFVNPGEDEVSRVVFYFNFSFLESFQGFVS 389  
DB 329 TRGSETNHYKRLAKSTLLIPLFGIHVIVFAFSP-EDAME--VOLFFELALGSFQGLVWA 385  
QY 390 VFYCFNLNSVRSAIRKRWHQ-----DKHSIRARVARAMSIP 427  
DB 386 VLYCFNLNGEVOLEQVKRQWHLQEPFLRPVAFNFSFNATNGPTHTSKASTQSR SIP 444

Search completed: March 16, 2006, 17:21:00  
Job time : 43 secs

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GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.  
OM protein - protein search, using sw model  
Run on: March 16, 2006, 17:13:03 ; Search time 231 Seconds  
(without alignments)  
1356.080 Million cell updates/sec  
Title: US-10-649-193-15  
Perfect score: 2381  
Sequence: 1 MGHQPQLRVKALLGLNP.....SIPTSPTRVFSHKSTAV 444

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5  
Searched: 2166443 seqs, 705528306 residues  
Total number of hits satisfying chosen parameters: 2166443  
Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries  
Database : Uniprot 05.80.\*  
1: uniprot\_sprot.\*  
2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2381	100.0	444	1	CRFR1_HUMAN
2	2324	97.6	447	2	CRNG71_HUMAN
3	2186.5	91.8	415	2	Q4QRJ1_HUMAN
4	2172.5	91.2	415	2	Q76LL8_MACMU
5	2146.5	90.2	415	2	Q8WM0_TUPGB
6	2137.5	89.8	415	1	CRFR1_MOUSE
7	2128.5	89.4	415	2	Q8K3R2_MESAU
8	2126.5	89.3	415	1	CRFR1_RAT
9	2126.5	89.3	415	2	Q9BGU4_BOVIN
10	2086.5	87.6	415	1	CRFR1_SHEEP
11	1945	81.7	420	1	CRFR1_CHICK
12	1817.5	76.3	445	2	Q98UC2_9TELE
13	1804	75.8	430	2	Q8AWA2_ONCKE
14	1796.5	75.5	415	1	CRFR1_XENLA
15	1789	75.1	416	2	Q8YV61_RANCA
16	1765	74.1	434	2	Q7T3S9_FUGRU
17	1741.5	73.1	428	2	Q98UC0_9TELE
18	1676.5	70.4	315	2	Q4JHT0_CERAE
19	1631	68.5	365	2	Q5GH80_ONCMY
20	1617.5	67.9	329	2	Q70JV6_CYPCA
21	1603.5	67.3	412	2	Q7Z222_CHICK
22	1580	66.4	437	2	Q8WML8_TUPGB
23	1576.5	66.2	414	2	Q8AWA1_ONCKE
24	1561	65.6	405	2	Q98UC1_9TELE
25	1559	65.5	410	2	Q8WML9_TUPGB
26	1550.5	65.1	411	1	CRFR2_RAT
27	1549.5	65.1	411	1	CRFR2_HUMAN
28	1549.5	65.1	411	2	Q4QRJ4_HUMAN
29	1543	64.8	431	1	CRFR2_MOUSE
30	1541.5	64.7	413	1	CRFR2_XENLA
31	1530.5	64.3	411	2	Q5GL24_MOUSE

32	1515.5	63.6	411	2	Q68Y60_RANCA	Q68Y60 rana catesb
33	1429	60.0	501	2	Q4S8L0_TETNG	Q4S8L0 tetraodon n
34	949	39.9	186	2	Q5PY21_EPICO	Q5PY21 epinephelus
35	743.5	31.2	277	2	Q8BJD9_MOUSE	Q8BJD9 m mus muscu
36	732.5	30.8	153	2	Q95L49_BOVIN	Q95L49 bos taurus
37	703	29.5	441	1	Q1HR_ACHDO	Q1HR93 acheta dome
38	686	28.8	150	2	Q5J877_ONCMY	Q5J877 oncorhynch
39	663.5	27.9	154	2	Q7TSA2_MESAU	Q7TSA2 mesocricetu
40	663	27.8	475	2	Q4V3E9_DROME	Q4V3E9 drosophila
41	662.5	27.8	454	2	Q7Q773_ANOGA	Q7Q773 anopheles g
42	662.5	27.8	504	2	Q9V716_DROME	Q9V716 drosophila
43	651.5	27.4	388	2	Q9V6C7_DROME	Q9V6C7 drosophila
44	638	26.8	641	2	Q6SAS2_9HEMI	Q6SAS2 nilaparvata
45	635	26.7	631	2	Q6SAS3_9HEMI	Q6SAS3 nilaparvata

ALIGNMENTS

RESULT 1  
ID CRFR1\_HUMAN STANDARD; PRT; 444 AA.  
AC P34998; Q13008; Q9UK64;  
DT 01-FEB-1994 (Rel. 28, Created)  
DT 01-FEB-1994 (Rel. 28, Last sequence update)  
DT 10-MAY-2005 (Rel. 47, Last annotation update)  
DE Corticotropin releasing factor receptor 1 precursor (CRF-R) (CRF1)  
DE (Corticotropin-releasing hormone receptor 1) (CRH-R 1).  
GN Name=CRHR1; Synonyms=CRFR, CRFR1, CRHR;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE [MRNA] (ISOFORMS CRF-R1 AND CRF-R2).  
RC TISSUE=Pituitary; PubMed=7692441;  
RX MEDLINE=94022296; PubMed=7692441; Vale W.M.;  
RA Chen R., Lewis K.A., Perrin M.H., Vale W.M.;  
RT "Expression cloning of a human corticotropin-releasing-factor receptor.";  
RL Proc. Natl. Acad. Sci. U.S.A. 90:8967-8971(1993).  
RN [2]  
RP NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM CRF-R2).  
RC TISSUE=Brain;  
RX MEDLINE=94063063; PubMed=8243652; DOI=10.1016/0014-5793(93)80427-V;  
RA Vita N., Laurent P., Lefort S., Chalon P., Lelias J.-M., Kaghad M.,  
le Fur G., Caput D., Ferrara P.;  
RT "Primary structure and functional expression of mouse pituitary and human brain corticotropin releasing factor receptors.";  
RL FEBS Lett. 335:1-5(1993).  
RN [3]  
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].  
RX MEDLINE=98434445; PubMed=9757017; DOI=10.1016/S0378-1119(98)00322-9;  
RA Sakai K., Yamada M., Horiba N., Wakui M., Demura H., Suda T.;  
RT "The genomic organization of the human corticotropin-releasing factor type-1 receptor.";  
RL Gene 219:125-130(1998).  
RN [4]  
RP NUCLEOTIDE SEQUENCE (ISOFORM CRF-R3).  
RC TISSUE=Hippocampus;  
RX MEDLINE=95110332; PubMed=7811272;  
RA Ross P.C., Kostas C.M., Ramabhadran T.V.;  
RT "A variant of the human corticotropin-releasing factor (CRF) receptor: cloning, expression and pharmacology.";  
RL Biochem. Biophys. Res. Commun. 205:1836-1842(1994).  
RN [5]  
RP NUCLEOTIDE SEQUENCE (ISOFORM CRF-R4).  
RX MEDLINE=20065650; PubMed=10598591; DOI=10.1210/me.13.12.2189;  
RA Grammatopoulos D.K., Dai Y., Randeve H.S., Levine M.A., Karteris E., Easton A.J., Hillhouse E.W.;  
RT "A novel spliced variant of the type 1 corticotropin-releasing hormone receptor with a deletion in the seventh transmembrane domain present

in the human pregnant term myometrium and fetal membranes.";  
 Mol. Endocrinol. 13:2189-2202(1999).  
 [6]  
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM CRF-R2).  
 TISSUE=Brain;  
 RA King M.M., Aronstam R.S., Sharma S.V.;  
 RT "cDNA clones of human proteins involved in signal transduction  
 RT sequenced by the Guthrie cDNA resource center (www.cdna.org).";  
 Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.  
 [7]  
 RP PROTEIN SEQUENCE OF 24-31, AND DISULFIDE BONDS.  
 RX PubMed=11425856; DOI=10.1074/jbc.M101838200;  
 RA Perrin M.H., Fleischer W.H., Kunitake K.S., Craig A.G., Koerber S.C.,  
 RA Cervini L.A., Rivter J.E., Gropp J.C., Greenwald J.,  
 RA Moller Nielsen S., Vale W.W.;  
 RT "Expression, purification, and characterization of a soluble form of  
 RT the first extracellular domain of the human type 1 corticotropin  
 RT releasing factor receptor.";  
 J. Biol. Chem. 276:31528-31534(2001).  
 CC -|- FUNCTION: This is a receptor for corticotropin releasing factor.  
 CC Shows high-affinity CRF binding. The activity of this receptor is  
 CC mediated by G proteins which activate adenylyl cyclase.  
 CC -|- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -|- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=4;  
 CC Name=CRF-R1;  
 CC IsoId=P34998-1; Sequence=Displayed;  
 CC Name=CRF-R2;  
 CC IsoId=P34998-2; Sequence=VSP\_001997;  
 CC Note=Major isoform;  
 CC Name=CRF-R3;  
 CC IsoId=P34998-3; Sequence=VSP\_001996, VSP\_001997;  
 CC Note=Does not bind to CRF with high affinity;  
 CC Name=CRF-R4; Synonyms=ID;  
 CC IsoId=P34998-4; Sequence=VSP\_001997, VSP\_001998;  
 CC -|- TISSUE SPECIFICITY: Predominantly expressed in the cerebellum,  
 CC pituitary, cerebral cortex and olfactory lobe.  
 CC -|- PTM: May be phosphorylated on Ser or Thr residues present in the  
 CC C-terminal part.  
 CC -|- SIMILARITY: Belongs to the G-protein coupled receptor 2 family.  
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use as long as its content is in no way modified and this statement is not  
 CC removed.  
 DR EMBL; L23333; AAA35719.1; -; mRNA.  
 DR EMBL; L23332; AAA35718.1; -; mRNA.  
 DR EMBL; X72304; CAA51052.1; -; mRNA.  
 DR EMBL; AF039523; AAC69993.1; -; Genomic\_DNA.  
 DR EMBL; AF039510; AAC69993.1; JOINED; Genomic\_DNA.  
 DR EMBL; AF039511; AAC69993.1; JOINED; Genomic\_DNA.  
 DR EMBL; AF039512; AAC69993.1; JOINED; Genomic\_DNA.  
 DR EMBL; AF039513; AAC69993.1; JOINED; Genomic\_DNA.  
 DR EMBL; AF039514; AAC69993.1; JOINED; Genomic\_DNA.  
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 DR EMBL; AF039522; AAC69993.1; JOINED; Genomic\_DNA.  
 DR EMBL; U16273; AAC50073.1; -; mRNA.  
 DR EMBL; AF180301; AAD52688.1; -; mRNA.  
 DR EMBL; AY457172; AAR19768.1; -; mRNA.  
 DR PIR; I38879; I38879.  
 DR PIR; I60975; A48260.  
 DR Ensembl; ENSG00000120088; Homo sapiens.  
 DR HGNC; HGNC:2357; CRHR1.  
 DR MIM; 122561; -.  
 DR GO; GO:0005887; C:integral to plasma membrane; TAS.  
 DR GO; GO:0005886; C:plasma membrane; TAS.  
 DR GO; GO:0015056; F:corticotropin-releasing factor receptor ac...; TAS.  
 DR GO; GO:0007190; P:adenylate cyclase activation; TAS.  
 DR GO; GO:0007188; P:G-protein coupled receptor protein signalin...; TAS.  
 DR GO; GO:0006955; P:immune response; TAS.  
 DR GO; GO:0007567; P:parturition; TAS.  
 DR GO; GO:0007565; P:pregnancy; NAS.  
 DR InterPro; IPR003052; CRF1\_receptor.  
 DR InterPro; IPR003051; CRF\_receptor.  
 DR InterPro; IPR000832; GPCR\_secretin.  
 DR InterPro; IPR001879; hormn\_receptor.  
 DR PANTHER; PTHR12011:SF16; CRF\_receptor; 2.  
 Pfam; PF00002; 7tm\_2; 1.  
 Pfam; PF02793; HRM; 1.  
 DR PRINTS; PRO1279; CRFRECEPTOR.  
 DR PRINTS; PRO1280; CRFRECEPTOR1.  
 DR PRINTS; PRO0249; GPCRSECRETIN.  
 DR SMART; SM00008; Hormr; 1.  
 DR PROSITE; PS00649; G\_PROTEIN\_RECEP\_F2\_1; 1.  
 DR PROSITE; PS00650; G\_PROTEIN\_RECEP\_F2\_2; 1.  
 DR PROSITE; PS00227; G\_PROTEIN\_RECEP\_F2\_3; 1.  
 DR PROSITE; PS00261; G\_PROTEIN\_RECEP\_F2\_4; 1.  
 KW Alternative splicing; Direct protein sequencing;  
 KW G-protein coupled receptor; Glycoprotein; Phosphorylation; Receptor;  
 KW Signal; Transducer; Transmembrane.  
 FT SIGNAL 1 23  
 FT CHAIN 24 444  
 FT 1. Corticotropin releasing factor receptor  
 FT TOPO\_DOM 24 121 Extracellular (Potential).  
 FT TRANSMEM 122 142 1 (Potential).  
 FT TOPO\_DOM 143 180 Cytoplasmic (Potential).  
 FT TRANSMEM 181 200 2 (Potential).  
 FT TOPO\_DOM 201 218 Extracellular (Potential).  
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 FT TOPO\_DOM 243 256 Cytoplasmic (Potential).  
 FT TRANSMEM 257 278 4 (Potential).  
 FT TOPO\_DOM 279 297 Extracellular (Potential).  
 FT TRANSMEM 298 320 5 (Potential).  
 FT TOPO\_DOM 321 343 Cytoplasmic (Potential).  
 FT TRANSMEM 344 378 6 (Potential).  
 FT TOPO\_DOM 379 398 Extracellular (Potential).  
 FT TRANSMEM 399 444 7 (Potential).  
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 FT CARBOHYD 45 45 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 78 78 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 90 90 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 98 98 N-linked (GlcNAc...) (Potential).  
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 FT DISULFID 44 87  
 FT DISULFID 68 102  
 FT VARSPPLIC 41 81  
 FT VARSPLIC 146 174  
 FT VARSPLIC 385 398  
 FT VARSPLIC 444 AA; 50719 MW; 7221AEP087AAED CRC64;  
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 -> D (in isoform CRF-R3).  
 /FTId=VSP\_001996.  
 Missing (in isoform CRF-R2, isoform CRF-  
 R3 and isoform CRF-R4).  
 /FTId=VSP\_001997.  
 Missing (in isoform CRF-R4).  
 /FTId=VSP\_001998.  
 Query Match 100.0%; Score 2381; DB 1; Length 444;  
 Best Local Similarity 100.0%; Pred. No. 3.6e-189;  
 Matches 444; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MGGHQLRLVKALLLGLNPNVSAIQDQCESLSLASISGLQCNASVDLIGTCWPRSPA 60  
 Db 1 MGGHQLRLVKALLLGLNPNVSAIQDQCESLSLASISGLQCNASVDLIGTCWPRSPA 60  
 QY 61 GQLVVRPCPAFFYGVRYNTTNNGYRECLANGWAARVNTYSECQILNEBKSKVHVAV 120  
 Db 61 GQLVVRPCPAFFYGVRYNTTNNGYRECLANGWAARVNTYSECQILNEBKSKVHVAV 120





RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC096836; AAH96836.1; -, mRNA.  
 KW Receptor.  
 SQ SEQUENCE 415 AA; 47671 MW; 81445283CCB34C6E CRC64;

Query Match 91.8%; Score 2186.5; DB 2; Length 415;  
 Best Local Similarity 93.5%; Pred. No. 4.7e-173;  
 Matches 415; Conservative 0; Mismatches 0; Indels 29; Gaps 1;

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QY 1 MGGHPQLRLVKALLGLNPNVSASLQDHCHESLSLASNISGLQCNASVDLIGTCWPRSPA 60
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DB 1 MGGHPQLRLVKALLGLNPNVSASLQDHCHESLSLASNISGLQCNASVDLIGTCWPRSPA 60
   |||||
QY 61 GQLVVRPCPAFFYGVRYNTNNGYRECLANGSAAARVNYSECQIILNEEKSKVHYHVAV 120
   |||||
DB 61 GQLVVRPCPAFFYGVRYNTNNGYRECLANGSAAARVNYSECQIILNEEKSKVHYHVAV 120
   |||||
QY 121 IINYLGHCHISLVALLVAFVFLRLRPGCTHWGDAQDALEVGAPWMSGAPFQVRSIRCLR 180
   |||||
DB 121 IINYLGHCHISLVALLVAFVFLRLR-----RSIRCLR 151
   |||||
QY 181 NIHWNLISAFILRNATWVQVLTMSPEVHQSNGVWCRLVTAAYNYPHVTNPFWMFGECC 240
   |||||
DB 152 NIHWNLISAFILRNATWVQVLTMSPEVHQSNGVWCRLVTAAYNYPHVTNPFWMFGECC 211
   |||||
QY 241 YLHTAIVLYTSTDRLRKWMPICIGWGVPPPIIIVAWAIGKLYYDNEKWCWFKRPGVYTDYI 300
   |||||
DB 212 YLHTAIVLYTSTDRLRKWMPICIGWGVPPPIIIVAWAIGKLYYDNEKWCWFKRPGVYTDYI 271
   |||||
QY 301 YQGPMLVLLINFIPLFNIVRIILMTKLRASTTSETIYQKRAKAVKATVLLPLLGITYMLFF 360
   |||||
DB 272 YQGPMLVLLINFIPLFNIVRIILMTKLRASTTSETIYQKRAKAVKATVLLPLLGITYMLFF 331
   |||||
QY 361 VNPGEDEVSRVVIYFNSFLESFQGFVSVFYCFNLSEVRSARIRKWHRWQDGHSTRARV 420
   |||||
DB 332 VNPGEDEVSRVVIYFNSFLESFQGFVSVFYCFNLSEVRSARIRKWHRWQDGHSTRARV 391
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QY 421 ARAMSIPTSPTRVSHSIKQSTAV 444
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DB 392 ARAMSIPTSPTRVSHSIKQSTAV 415
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## RESULT 4

Q76LL8 MACMU  
 ID Q76LL8\_MACMU PRELIMINARY; PRT; 415 AA.  
 AC Q76LL8,  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DE Corticotropin releasing factor receptor type 1.  
 GN Names=CRF1;  
 OS Macaca mulatta (Rhesus macaque).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 OC Cercopitheciidae; Cercopitheciinae; Macaca.  
 OX NCBI\_TaxID=9544;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Ohida Y., Ikeda Y., Chaki S., Okuyama S.;  
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AB078141; BAD02831.1; -, mRNA.  
 DR GO; GO:0016021; C:integral to membrane; IEA.  
 DR GO; GO:0016020; C:membrane; IEA.  
 DR GO; GO:0004930; F:G-protein coupled receptor activity; IEA.  
 DR GO; GO:0004872; F:receptor activity; IEA.  
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.  
 DR InterPro; IPR003052; CRF1 receptor.  
 DR InterPro; IPR003051; CRF receptor.  
 DR InterPro; IPR000832; GPCR\_secretin.  
 DR InterPro; IPR001879; hormn\_receptor.  
 DR Pfam; PF00002; 7tm\_2; 1.  
 DR Pfam; PF02793; HRM; 1.  
 DR PRINTS; PR01279; CRFRECEPTOR.

DR PRINTS; PR01280; CRFRECEPTOR1.  
 DR PRINTS; PR00249; GPCRSECRETIN.  
 DR SMART; SM00008; Hormr; 1.  
 DR PROSITE; PS00649; G\_PROTEIN\_RECEP\_F2\_1; 1.  
 DR PROSITE; PS00650; G\_PROTEIN\_RECEP\_F2\_2; 1.  
 DR PROSITE; PS0227; G\_PROTEIN\_RECEP\_F2\_3; 1.  
 DR PROSITE; PS0261; G\_PROTEIN\_RECEP\_F2\_4; 1.  
 KW Receptor.  
 SQ SEQUENCE 415 AA; 47784 MW; 84C530DEC6DA97AD CRC64;

Query Match 91.2%; Score 2172.5; DB 2; Length 415;  
 Best Local Similarity 93.0%; Pred. No. 6.9e-172;  
 Matches 413; Conservative 0; Mismatches 2; Indels 29; Gaps 1;

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QY 1 MGGHPQLRLVKALLGLNPNVSASLQDHCHESLSLASNISGLQCNASVDLIGTCWPRSPA 60
   |||||
DB 1 MGGHPQLRLVKALLGLNPNVSASLQDHCHESLSLASNISGLQCNASVDLIGTCWPRSPA 60
   |||||
QY 61 GQLVVRPCPAFFYGVRYNTNNGYRECLANGSAAARVNYSECQIILNEEKSKVHYHVAV 120
   |||||
DB 61 GQLVVRPCPAFFYGVRYNTNNGYRECLANGSAAARVNYSECQIILNEEKSKVHYHVAV 120
   |||||
QY 121 IINYLGHCHISLVALLVAFVFLRLRPGCTHWGDAQDALEVGAPWMSGAPFQVRSIRCLR 180
   |||||
DB 121 IINYLGHCHISLVALLVAFVFLRLR-----RSIRCLR 151
   |||||
QY 181 NIHWNLISAFILRNATWVQVLTMSPEVHQSNGVWCRLVTAAYNYPHVTNPFWMFGECC 240
   |||||
DB 152 NIHWNLISAFILRNATWVQVLTMSPEVHQSNGVWCRLVTAAYNYPHVTNPFWMFGECC 211
   |||||
QY 241 YLHTAIVLYTSTDRLRKWMPICIGWGVPPPIIIVAWAIGKLYYDNEKWCWFKRPGVYTDYI 300
   |||||
DB 212 YLHTAIVLYTSTDRLRKWMPICIGWGVPPPIIIVAWAIGKLYYDNEKWCWFKRPGVYTDYI 271
   |||||
QY 301 YQGPMLVLLINFIPLFNIVRIILMTKLRASTTSETIYQKRAKAVKATVLLPLLGITYMLFF 360
   |||||
DB 272 YQGPMLVLLINFIPLFNIVRIILMTKLRASTTSETIYQKRAKAVKATVLLPLLGITYMLFF 331
   |||||
QY 361 VNPGEDEVSRVVIYFNSFLESFQGFVSVFYCFNLSEVRSARIRKWHRWQDGHSTRARV 420
   |||||
DB 332 VNPGEDEVSRVVIYFNSFLESFQGFVSVFYCFNLSEVRSARIRKWHRWQDGHSTRARV 391
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QY 421 ARAMSIPTSPTRVSHSIKQSTAV 444
   |||||
DB 392 ARAMSIPTSPTRVSHSIKQSTAV 415
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## RESULT 5

Q8WMM0 TUPGB  
 ID Q8WMM0\_TUPGB PRELIMINARY; PRT; 415 AA.  
 AC Q8WMM0,  
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE Corticotropin releasing factor type 1 receptor.  
 GN Names=crf1;  
 OS Tupiaia glis belangeri (Common tree shrew).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Scandentia; Tupaiidae; Tupiaia.  
 OX NCBI\_TaxID=37347;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA MEDLINE; 99067019; PubMed=9851694;  
 RX Palchaudhuri M.R., Wille S., Mevenkamp G., Spiess J., Fuchs E.,  
 RA Bautzenberg F.M.;  
 RT "Corticotropin-releasing factor receptor type 1 from Tupiaia belangeri:  
 RT cloning, functional expression and tissue distribution.";  
 RL Eur. J. Biochem. 258:78-84(1998).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Bautzenberg F.M.;  
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AJ42241; CAD19577.1; -, mRNA.

DR GO: GO:0016021; C: integral to membrane; IEA.  
DR GO: GO:0016020; C: membrane; IEA.  
DR GO: GO:0004930; P: G-protein coupled receptor activity; IEA.  
DR GO: GO:0004872; F: receptor activity; IEA.  
DR GO: GO:0007186; P: G-protein coupled receptor protein signalin. .; IEA.  
DR InterPro: IPR003052; CRF1 receptor.  
DR InterPro: IPR003051; CRF1 receptor.  
DR InterPro: IPR000832; GPCR secretin.  
DR InterPro: IPR001879; hormn\_receptor.  
DR Pfam: PF00002; 7tm\_2; 1.  
DR Pfam: PF02793; HRM; 1.  
DR PRINTS; PR01279; CRFRECEPTOR.  
DR PRINTS; PR01280; CRFRECEPTOR.  
DR PRINTS; PR00249; GPCRSECRETIN.  
DR SMART; SM00008; Hormr; 1.  
DR PROSITE; PS00649; G\_PROTEIN\_RECEP\_F2\_1; 1.  
DR PROSITE; PS00650; G\_PROTEIN\_RECEP\_F2\_2; 1.  
DR PROSITE; PS0227; G\_PROTEIN\_RECEP\_F2\_3; 1.  
DR PROSITE; PS0261; G\_PROTEIN\_RECEP\_F2\_4; 1.  
KW Receptor.  
SQ SEQUENCE 415 AA; 47685 MW; 97B9ABE050AC08D CRC64;  
Query Match 90.2%; Score 2146.5; DB 2; Length 415;  
Best Local Similarity 91.7%; Pred. No. 1e-169;  
Matches 407; Conservative 3; Mismatches 5; Indels 29; Gaps 1;  
QY 1 MGGHPQLRLVKALLGLNPVSASLQDQHCESLSLANISGLQCNASVDLIGTCWPRSPA 60  
DB 1 MGRGPHRLRLVKALLGLNPVSASLQDQHCESLPTSNVSGLQCNASVDLIGTCWPRSPA 60  
QY 61 GQLVVRPCAPFYGVRYNTNNGYRECLANGSWAARVNYSECOILNEEKSKVHVAV 120  
DB 61 GQLVVRPCAPFYGVRYNTNNGYRECLANGSWAARVNYSECOILNEEKSKVHVAV 120  
QY 121 IINVLGHCSLVALLVAFVFLRLRPGCTHWGDAQDGALEVGAPWPGAPQVRRSIRCLR 180  
DB 121 IINVLGHCSLVALLVAFVFLRLR-----RSIRCLR 151  
QY 181 NIHWNLISAFILRNATFVYVQLTMSPEVHQSNVGCRLVTAAYNPVPHVTFNFMFGEGC 240  
DB 152 NIHWNLISAFILRNATFVYVQLTMSPEVHQSNVGCRLVTAAYNPVPHVTFNFMFGEGC 211  
QY 241 YLHTAIVLTSTDLRLKWMFCICGWGVPFPIIIVAWAIGKLYYNEKCFGRGVTVDYI 300  
DB 212 YLHTAIVLTSTDLRLKWMFCICGWGVPFPIIIVAWAIGKLYYNEKCFGRGVTVDYI 271  
QY 301 YQGPMLVLLINFIELFNIRIILMTKLRASTTSETIQYKAVKATLVLLPLLGITYMLFF 360  
DB 272 YQGPMLVLLINFIELFNIRIILMTKLRASTTSETIQYKAVKATLVLLPLLGITYMLFF 331  
QY 361 VNPGEDEVSRVFIYFNFSFLESFGQFPVSVFYCFNLSEVSAIRKRWHRWQDKHSIRARV 420  
DB 332 VNPGEDEVSRVFIYFNFSFLESFGQFPVSVFYCFNLSEVSAIRKRWHRWQDKHSIRARV 391  
QY 421 ARAMSIPTSPTRVSHSIKOSTAV 444  
DB 392 ARAMSIPTSPTRVSHSIKOSTAV 415  
RESULT 6  
ID CRFR1 MOUSE STANDARD; PRT; 415 AA.  
AC P35347;  
DT 01-JUN-1994 (Rel. 29, Created)  
DT 01-JUN-1994 (Rel. 29, Last sequence update)  
DT 10-MAY-2005 (Rel. 47, Last annotation update)  
DE Corticotropin releasing factor receptor 1 precursor (CRF-R) (CRF1)  
GN Names=Crhr1; Synonyms=Crhr;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muridea; Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Pituitary;  
RX MEDLINE=94063063; PubMed=8243652; DOI=10.1016/0014-5793(93)80427-V;  
RA Vita N., Laurent P., Lefort S., Chalon P., Lelias J.-M., Kaghad M.,  
le Fur G., Caput D., Ferrara P.;  
RT "Primary structure and functional expression of mouse pituitary and  
human brain corticotrophin releasing factor receptors.";  
RL FEBS Lett. 335:1-5(1993).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=ILS and ISS;  
RX MEDLINE=21363810; PubMed=11471062; DOI=10.1007/s00335-001-1001-x;  
RA Ehringer M.A., Thompson J., Conroy O., Xu Y., Yang F., Caniff J.,  
Beeson M., Gordon L., Bennett B., Johnson T.E., Sikela J.M.;  
RT "High-throughput sequence identification of gene coding variants  
within alcohol-related QTLs.";  
RL Mamm. Genome 12:657-663(2001).  
CC -1- FUNCTION: This is a receptor for corticotropin releasing factor.  
CC mediated by G proteins which activate adenylyl cyclase.  
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
CC in placenta, peripheral blood, lymphocytes, kidney and liver.  
CC -1- PTM: Carboxyl-terminal Ser or Thr residues may be phosphorylated.  
CC -1- SIMILARITY: Belongs to the G-protein coupled receptor 2 family.  
CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use as long as its content is in no way modified and this statement is not  
CC removed.  
DR ENBL; X72305; CAA51053.1; -; mRNA.  
DR ENBL; AF483484; AAL90758.1; -; mRNA.  
DR ENBL; AF483485; AAL90759.1; -; mRNA.  
DR PIR; S39535; S39535.  
DR Ensembl; ENSMUSG0000018634; Mus musculus.  
DR MGI; MGI:88498; Crhr1.  
DR GO: GO:0005615; C: extracellular space; TAS.  
DR GO: GO:0016021; C: integral to membrane; TAS.  
DR GO: GO:0010566; F: corticotrophin-releasing factor receptor ac. .; IMP.  
DR GO: GO:0007610; P: behavior; IMP.  
DR GO: GO:0006950; P: response to stress; IMP.  
DR InterPro: IPR003052; CRF1 receptor.  
DR InterPro: IPR003051; CRF receptor.  
DR InterPro: IPR000832; GPCR secretin.  
DR InterPro: IPR001879; hormn\_receptor.  
DR PANTHER; PTHR12011:SF16; CRF\_receptor; 1.  
DR Pfam; PF00002; 7tm\_2; 1.  
DR Pfam; PF02793; HRM; 1.  
DR PRINTS; PR01279; CRFRECEPTOR.  
DR PRINTS; PR01280; CRFRECEPTOR.  
DR PRINTS; PR00249; GPCRSECRETIN.  
DR SMART; SM00008; Hormr; 1.  
DR PROSITE; PS00649; G\_PROTEIN\_RECEP\_F2\_1; 1.  
DR PROSITE; PS00650; G\_PROTEIN\_RECEP\_F2\_2; 1.  
DR PROSITE; PS0227; G\_PROTEIN\_RECEP\_F2\_3; 1.  
DR PROSITE; PS0261; G\_PROTEIN\_RECEP\_F2\_4; 1.  
KW G-protein coupled receptor; Glycoprotein; Phosphorylation; Receptor;  
KW Signal; Transducer; Transmembrane.  
FT SIGNAL 1 23 Potential.  
FT CHAIN 24 415 Corticotropin releasing factor receptor  
FT FT 1.  
FT TOPO\_DOM 24 121 Extracellular (Potential).  
FT TRANSMEM 122 142 1 (Potential).  
FT TOPO\_DOM 143 151 Cytoplasmic (Potential).  
FT TRANSMEM 152 171 2 (Potential).  
FT TOPO\_DOM 172 189 Extracellular (Potential).  
FT TRANSMEM 190 213 3 (Potential).  
FT TOPO\_DOM 214 227 Cytoplasmic (Potential).  
FT TRANSMEM 228 249 4 (Potential).

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FT TOPO_DOM 250 268 Extracellular (Potential).
FT TRANSMEM 269 291 5 (Potential).
FT TOPO_DOM 292 314 Cytoplasmic (Potential).
FT TRANSMEM 315 334 6 (Potential).
FT TOPO_DOM 335 349 Extracellular (Potential).
FT TRANSMEM 350 369 7 (Potential).
FT TOPO_DOM 370 415 Cytoplasmic (Potential).
FT CARBOHYD 38 38 N-linked (GLNAC. . .) (Potential).
FT CARBOHYD 45 45 N-linked (GLNAC. . .) (Potential).
FT CARBOHYD 78 78 N-linked (GLNAC. . .) (Potential).
FT CARBOHYD 90 90 N-linked (GLNAC. . .) (Potential).
FT CARBOHYD 98 98 N-linked (GLNAC. . .) (Potential).
FT DISULFID 30 54 By similarity.
FT DISULFID 44 87 By similarity.
FT DISULFID 68 102 By similarity.
SQ SEQUENCE 415 AA; 47769 MW; 8143BD6DICA070 CRC64;

Query Match 89.8%; Score 2137.5; DB 1; Length 415;
Best Local Similarity 91.2%; Pred. No. 5.6e-169;
Matches 405; Conservative 4; Mismatches 6; Indels 29; Gaps 1;

QY 1 MGHHPQLRLVKALLLGLNPVSASLQDQCHCESLSLASNISGLQCNASVDLIGTCWPRSPA 60
DB 1 MGQRPLQLRVKALLLGLNPVSTSLQDQCHCESLSLASNVSGLCNASVDLIGTCWPRSPA 60
QY 61 GQLVVRPCPAFFYGVRYNTTNGYRECLANGSWAARVNYSECOEILNEEKSKVHYHVAV 120
DB 61 GQLVVRPCPAFFYGVRYNTTNGYRECLANGSWAARVNYSECOEILNEEKSKVHYHVAV 120
QY 121 IINYLGHGISLVALLVAFVFLRLRPGCTHWGQDADGALEVGAPWMSGAPFQVRRSIRCLR 180
DB 121 IINYLGHGISLVALLVAFVFLRLRPGCTHWGQDADGALEVGAPWMSGAPFQVRRSIRCLR 180
QY 181 NIHNWNLISAFILRNATWFWVQLTWSPVHQSNVGCRLVTAAYNFHVTFNPFMFGECC 240
DB 152 NIHNWNLISAFILRNATWFWVQLTWSPVHQSNVGCRLVTAAYNFHVTFNPFMFGECC 211
QY 241 YLHTAIVLTYSTDLRLKWMFICIGWGVPPPIIVAMAIGKLYYDNEKCFKRGVGVTDYI 300
DB 212 YLHTAIVLTYSTDLRLKWMFVCIWGVPPPIIVAMAIGKLYYDNEKCFKRGVGVTDYI 271
QY 301 YQGPMLVLLINFIPLFNIVIRILMTKLRASTTSETTIQYRKAVKATLVLLPLLGITYMLFF 360
DB 272 YQGPMLVLLINFIPLFNIVIRILMTKLRASTTSETTIQYRKAVKATLVLLPLLGITYMLFF 331
QY 361 VNPGEDEVSRVVIYFNSFLESQGFVSVFYCFNLSEVRSAIRKRWHRWQDKHSIRARV 420
DB 332 VNPGEDEVSRVVIYFNSFLESQGFVSVFYCFNLSEVRSAIRKRWHRWQDKHSIRARV 391
QY 421 ARAMSIPTSPTRVSPHSIKQSTAV 444
DB 392 ARAMSIPTSPTRVSPHSIKQSTAV 415

RESULT 7
Q8K3R2_MESAU PRELIMINARY; PRT; 415 AA.
AC Q8K3R2;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Type-1 corticotropin-releasing hormone receptor alpha isoform.
GN Name-CRH-R1;
OS Mesocricetus auratus (Golden hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Cricetinae; Mesocricetus.
OX NCBI_TaxID=10036;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Pisarchik A.V., Slominski A.;
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY034599; AAK59707.1; -, mRNA.

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DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004930; F:G-protein coupled receptor activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0007186; F:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR003052; CRF1_receptor.
DR InterPro; IPR000832; GPCR_receptor.
DR InterPro; IPR001879; hormn_receptor.
DR Pfam; PF00002; 7tm_2; 1.
DR Pfam; PF02793; HRM; 1.
DR PRINTS; PR01279; CRPRECEPTOR.
DR PRINTS; PR01280; CRPRECEPTOR1.
DR PRINTS; PR00249; GPCRSECRETIN.
DR SMART; SM00008; Hormb; 1.
DR PROSITE; PS00649; G_PROTEIN_RECEP_F2_1; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; 1.
DR PROSITE; PS00327; G_PROTEIN_RECEP_F2_3; 1.
DR PROSITE; PS00261; G_PROTEIN_RECEP_F2_4; 1.
KW Receptor.
SQ SEQUENCE 415 AA; 47702 MW; 500B4DD617E5F19E CRC64;

Query Match 89.4%; Score 2128.5; DB 2; Length 415;
Best Local Similarity 90.8%; Pred. No. 3.1e-168;
Matches 403; Conservative 5; Mismatches 7; Indels 29; Gaps 1;

QY 1 MGHHPQLRLVKALLLGLNPVSASLQDQCHCESLSLASNISGLQCNASVDLIGTCWPRSPA 60
DB 1 MGQRPLQLRVKALLLGLNPVSTSLQDQCHCESLSLASNVSGPCNASVDLIGTCWPRSPA 60
QY 61 GQLVVRPCPAFFYGVRYNTTNGYRECLANGSWAARVNYSECOEILNEEKSKVHYHVAV 120
DB 61 GQLVVRPCPAFFYGVRYNTTNGYRECLANGSWAARVNYSECOEILNEEKSKVHYHVAV 120
QY 121 IINYLGHGISLVALLVAFVFLRLRPGCTHWGQDADGALEVGAPWMSGAPFQVRRSIRCLR 180
DB 121 IINYLGHGISLVALLVAFVFLRLRPGCTHWGQDADGALEVGAPWMSGAPFQVRRSIRCLR 180
QY 181 NIHNWNLISAFILRNATWFWVQLTWSPVHQSNVGCRLVTAAYNFHVTFNPFMFGECC 240
DB 152 NIHNWNLISAFILRNATWFWVQLTWSPVHQSNVGCRLVTAAYNFHVTFNPFMFGECC 211
QY 241 YLHTAIVLTYSTDLRLKWMFICIGWGVPPPIIVAMAIGKLYYDNEKCFKRGVGVTDYI 300
DB 212 YLHTAIVLTYSTDLRLKWMFVCIWGVPPPIIVAMAIGKLYYDNEKCFKRGVGVTDYI 271
QY 301 YQGPMLVLLINFIPLFNIVIRILMTKLRASTTSETTIQYRKAVKATLVLLPLLGITYMLFF 360
DB 272 YQGPMLVLLINFIPLFNIVIRILMTKLRASTTSETTIQYRKAVKATLVLLPLLGITYMLFF 331
QY 361 VNPGEDEVSRVVIYFNSFLESQGFVSVFYCFNLSEVRSAIRKRWHRWQDKHSIRARV 420
DB 332 VNPGEDEVSRVVIYFNSFLESQGFVSVFYCFNLSEVRSAIRKRWHRWQDKHSIRARV 391
QY 421 ARAMSIPTSPTRVSPHSIKQSTAV 444
DB 392 ARAMSIPTSPTRVSPHSIKQATAV 415

RESULT 8
CRFR1_RAT
ID CRFR1_RAT STANDARD; PRT; 415 AA.
AC P35353;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Corticotropin-releasing factor receptor 1 precursor (CRF-R) (CRF1)
DE (Corticotropin-releasing hormone receptor 1) (CRH-R 1).
DE Name-Crhrl; Synonyms-Crhrl;
GN Rattus norvegicus (Rat).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidae; Muridae; Murinae; Rattus.

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OX NCBI\_TaxID=10116;  
RN NUCLEOTIDE SEQUENCE.  
RP STRAIN=Sprague-Dawley; TISSUE=Brain;  
RX MEDLINE=94062694; PubMed=8243336; DOI=10.1210/en.133.6.3058;  
RA Perrin M.H., Donaldson C.J., Chen R., Lewis K.A., Vale W.W.;  
RT "Cloning and functional expression of a rat brain corticotropin  
releasing factor (CRF) receptor.";  
RL Endocrinology 133:3058-3061(1993).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=Sprague-Dawley;  
RX MEDLINE=9409969; PubMed=8274282; DOI=10.1016/0896-6273(93)90230-O;  
RA Chang C.P., Pearce R.V. II, O'Connell S., Rosenfeld M.G.;  
RT "Identification of a seven transmembrane helix receptor for  
corticotropin-releasing factor and sauvagine in mammalian brain.";  
RL Neuron 11:1187-1195(1993).  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Testis;  
RX MEDLINE=96278921; PubMed=8662941; DOI=10.1074/jbc.271.24.14519;  
RA Tsai-Morris C.-H., Buczeko E., Geng Y., Gamboa-Pinto A., Dufau M.L.;  
RT "The genomic structure of the rat corticotropin releasing factor  
receptor. A member of the class II G protein-coupled receptors.";  
RL J. Biol. Chem. 271:14519-14525(1996).  
RN [4]  
RP DISULFIDE BONDS, AND CARBOHYDRATE-LINKAGE SITES.  
RX MEDLINE=21451158; PubMed=11567096; DOI=10.1110/ps.12101;  
RA Hofmann B.A., Sydow S., Jahn O., van Werven L., Liepold T., Eckart K.,  
RA Spiess J.;  
RT "Functional and protein chemical characterization of the N-terminal  
domain of the rat corticotropin-releasing factor receptor 1.";  
RL Protein Sci. 10:2050-2062(2001).  
CC -!- FUNCTION: This is a receptor for corticotropin releasing factor.  
CC Shows high-affinity CRF binding. The activity of this receptor is  
mediated by G proteins which activate adenylyl cyclase.  
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
CC -!- TISSUE SPECIFICITY: Entire nervous system.  
CC -!- FTM: Carboxyl-terminal Ser or Thr residues may be phosphorylated.  
CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 2 family.  
CC -----  
CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
between the Swiss Institute of Bioinformatics and the EMBL outstation -  
the European Bioinformatics Institute. There are no restrictions on its  
use as long as its content is in no way modified and this statement is not  
removed.  
CC -----  
DR EMBL; L24096; -; NOT ANNOTATED CDS; mRNA.  
DR EMBL; L25438; AAAL6441.1; -; Genomic DNA.  
DR EMBL; US3498; AAC3519.1; JOINED; Genomic DNA.  
DR EMBL; US3486; AAC3519.1; JOINED; Genomic DNA.  
DR EMBL; US3487; AAC3519.1; JOINED; Genomic DNA.  
DR EMBL; US3488; AAC3519.1; JOINED; Genomic DNA.  
DR EMBL; US3489; AAC3519.1; JOINED; Genomic DNA.  
DR EMBL; US3490; AAC3519.1; JOINED; Genomic DNA.  
DR EMBL; US3491; AAC3519.1; JOINED; Genomic DNA.  
DR EMBL; US3492; AAC3519.1; JOINED; Genomic DNA.  
DR EMBL; US3493; AAC3519.1; JOINED; Genomic DNA.  
DR EMBL; US3494; AAC3519.1; JOINED; Genomic DNA.  
DR EMBL; US3495; AAC3519.1; JOINED; Genomic DNA.  
DR EMBL; US3496; AAC3519.1; JOINED; Genomic DNA.  
DR EMBL; US3497; AAC3519.1; JOINED; Genomic DNA.  
DR F01; I58144; I58144.  
DR Ensembl; ENSRNOG0000004900; Rattus norvegicus.  
DR RGD; 61276; Crhl.  
DR GO; GO:0004930; F-G-protein coupled receptor activity; IDA.  
DR GO; GO:0007188; P-G-protein signaling, coupled to cAMP nucleo. .; IDA.  
DR GO; GO:0007218; P-neuropeptide signaling pathway; IDA.  
DR InterPro; IPR003052; CRF1 receptor.  
DR InterPro; IPR003051; CRF receptor.  
DR InterPro; IPR000832; GPCR\_secretin.  
DR InterPro; IPR01879; hormn\_receptor.  
DR PANTHER; PTHR12011:SF16; CRF\_receptor; 1.

DR Pfam; PF00002; 7tm\_2; 1.  
DR Pfam; PF02793; HRM; 1.  
DR PRINTS; PRO1279; CRFRECEPTOR.  
DR PRINTS; PRO1280; GPCRRECEPTOR1.  
DR PRINTS; PRO0249; GPCRSECRETIN.  
DR SMART; SM00008; Hormr; 1.  
DR PROSITE; PS00649; G\_PROTEIN\_RECEP\_F2\_1; 1.  
DR PROSITE; PS00650; G\_PROTEIN\_RECEP\_F2\_2; 1.  
DR PROSITE; PS0227; G\_PROTEIN\_RECEP\_F2\_3; 1.  
DR PROSITE; PS0261; G\_PROTEIN\_RECEP\_F2\_4; 1.  
KW G-protein coupled receptor; Glycoprotein; Phosphorylation; Receptor;  
KW Signal; Transducer; Transmembrane.  
FT SIGNAL 1 23  
FT CHAIN 24 415  
FT -----  
FT FT Corticotropin releasing factor receptor  
FT 1.  
FT TOPO\_DOM 24 121 Extracellular (Potential).  
FT TRANSMEM 122 142 1 (Potential).  
FT TOPO\_DOM 143 151 Cytoplasmic (Potential).  
FT TRANSMEM 152 171 2 (Potential).  
FT TOPO\_DOM 172 189 Extracellular (Potential).  
FT TRANSMEM 190 213 3 (Potential).  
FT TOPO\_DOM 214 227 Cytoplasmic (Potential).  
FT TRANSMEM 228 249 4 (Potential).  
FT TOPO\_DOM 250 268 Extracellular (Potential).  
FT TRANSMEM 269 291 5 (Potential).  
FT TOPO\_DOM 292 314 Cytoplasmic (Potential).  
FT TRANSMEM 315 334 6 (Potential).  
FT TOPO\_DOM 335 349 Extracellular (Potential).  
FT TRANSMEM 350 369 7 (Potential).  
FT TOPO\_DOM 370 415 Cytoplasmic (Potential).  
FT CARBOHYD 38 38 N-linked (GlcNAc. .).  
FT CARBOHYD 45 45 N-linked (GlcNAc. .).  
FT CARBOHYD 78 78 N-linked (GlcNAc. .).  
FT CARBOHYD 98 98 N-linked (GlcNAc. .).  
FT DISULFID 30 54 N-linked (GlcNAc. .).  
FT DISULFID 44 87  
FT DISULFID 68 102  
FT SEQUENCE 415 AA; 47842 MW; 48D6704B3D4C013 CRC64;  
Query Match 89.3%; Score 2126.5; DB 1; Length 415;  
Best Local Similarity 90.8%; Pred. No. 4.6e-168;  
Matches 403; Conservative 5; Mismatches 7; Indels 29; Gaps 1;  
QY 1 MGHHPQLRLVKALLLGLNPVSASLQDQHCESLSLASNISGLQCNASVDLIGTCWRPSA 60  
DB 1 MGRRPQLRLVKALLLGLNPVSTSLQDQCENLSLTSNVSLQCNASVDLIGTCWRPSA 60  
QY 61 GQLVVRPCAPFYGVYRNTNNGYRCLANGSWAARVNTSECOILNEEKSKVHYHVAV 120  
DB 61 GQLVVRPCAPFYGVYRNTNNGYRCLANGSWAARVNTSECOILNEEKSKVHYHVAV 120  
QY 121 IINYLGHCHLSVALLVAVFLRLRPGCTHWGDAQDALEVGAPWSGAPQVRRSIRCLR 180  
DB 121 IINYLGHCHLSVALLVAVFLRLRPGCTHWGDAQDALEVGAPWSGAPQVRRSIRCLR 180  
QY 181 NIHNWNLISAFILRNATFWVQLTMSPEVHQSNVGCRLVTAAYNYPHVTFNFMFEGGC 240  
DB 152 NIHNWNLISAFILRNATFWVQLTMSPEVHQSNVGCRLVTAAYNYPHVTFNFMFEGGC 211  
QY 241 YLHTAIVLTYSTDRLRKWFICIGWGPPIIIVAWAIGKLYYDNEKWCWFGKRGVYTDYI 300  
DB 212 YLHTAIVLTYSTDRLRKWFICIGWGPPIIIVAWAIGKLYYDNEKWCWFGKRGVYTDYI 271  
QY 301 YQGPMILVLLINFIPLFNIRIIMTKLRSTTSETIQYRKAVKATVLLPLLIGITYMLFF 360  
DB 272 YQGPMILVLLINFIPLFNIRIIMTKLRSTTSETIQYRKAVKATVLLPLLIGITYMLFF 331  
QY 361 VNFGEDEVSRVPIYFNPSFLESFGQFVSVFYFCFLNSVEVSAIRKRWHRWQDKHSIRARV 420  
DB 332 VNFGEDEVSRVPIYFNPSFLESFGQFVSVFYFCFLNSVEVSAIRKRWHRWQDKHSIRARV 391  
QY 421 ARAMSIPTSPTRVSVFHSIKQSTAV 444

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|||||
392 ARAMSIPTSPTRVSPHSHKSTAV 415

RESULT 9
Q9BGU4 BOVIN
ID Q9BGU4 BOVIN PRELIMINARY; PRT; 415 AA.
AC Q9BGU4
DT 01-JUN-2001 (T-EMBLrel. 17, Created)
DT 01-JUN-2001 (T-EMBLrel. 17, Last sequence update)
DT 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)
DE Corticotropin-releasing hormone receptor.
GN Name=CRFR;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Holstein;
RA Takata M., Sekikawa K.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB05434; BAB21864.1; -; mRNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004930; F:G-protein coupled receptor activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPRO03052; CRF1 receptor.
DR InterPro; IPRO03051; GPCR secretin.
DR InterPro; IPRO00832; GPCR secretin.
DR InterPro; IPRO01879; hormn_receptor.
DR Pfam; PF00002; 7tm_2; 1.
DR Pfam; PF02793; HRM; 1.
DR PRINTS; PR01279; CRFRECEPTOR.
DR PRINTS; PR01280; CRFRECEPTOR1.
DR PRINTS; PR00249; GPCRSECRETIN.
DR SMART; SM00008; Hormr; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; 1.
DR PROSITE; PS02277; G_PROTEIN_RECEP_F2_3; 1.
DR PROSITE; PS50261; G_PROTEIN_RECEP_F2_4; 1.
KW Receptor.
SQ SEQUENCE. 415 AA; 47754 MW; 4A54A3DCE6CF2319 CRC64;

Query Match 89.3%; Score 2126.5; DB 2; Length 415;
Best Local Similarity 90.5%; Pred. No. 4.6e-168;
Matches 402; Conservative 7; Mismatches 6; Indels 29; Gaps 1;

QY 1 MCGHPQLRLVKALLLGLNPVSALQDQHCESLSLASNTSGLOCNASVDLIGTCWPRSPA 60
DB 1 MGRRPQLRLVKALLLGLNLSISASLQDQHCESLSVASNSVGLQCNASVDLIGTCWQPSA 60

QY 61 GQLVVRPCPAFFYGVRYNTTNGYRECLANGSWAARVNSYSECQILNEEKSKVHYHVA 120
DB 61 GQLVVRPCLVFFYGVRYNTTNGYRECLANGTWAARVNSYSECQILNEEKSKVHYHVA 120

QY 121 IINYLGHCSLVALLVAFVLFLRLPGCTHWGQDQDALEVGAPNSGAPPQVRRSTRCLR 180
DB 121 IINYLGHCSLVALLVAFVLFLRLPGCTHWGQDQDALEVGAPNSGAPPQVRRSTRCLR 180

QY 121 IINYLGHCSLVALLVAFVLFLRLPGCTHWGQDQDALEVGAPNSGAPPQVRRSTRCLR 151
DB 121 IINYLGHCSLVALLVAFVLFLRLPGCTHWGQDQDALEVGAPNSGAPPQVRRSTRCLR 151

QY 181 NIHWNLISAFILRNATFVVQVTMSPEVHOSNVGCRVLTAAYNFVHTNPFMMFGEGC 240
DB 181 NIHWNLISAFILRNATFVVQVTMSPEVHOSNVGCRVLTAAYNFVHTNPFMMFGEGC 211

QY 241 YLHTAIVLTSTDLRLKRMFICIGWGPFPPIIVAMAIGKLYYDNKCFKRGVYTDYI 300
DB 212 YLHTAIVLTSTDLRLKRMFICIGWGPFPPIIVAMAIGKLYYDNKCFKRGVYTDYI 271

QY 301 YQGPMLVLLINIFLNFIVNIRILMTKLRASTSETTQYRKAVKATVLLPLLIGITVMLFF 360
DB 272 YQGPMLVLLINIFLNFIVNIRILMTKLRASTSETTQYRKAVKATVLLPLLIGITVMLFF 331
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QY 361 VNPGEDEVSRVVFIYFNFSFLESFQGFVSVFCFLNSELVRSAIRKRWHRWQDKHSIRARV 420
DB 332 VNPGEDEVSRVVFIYFNFSFLESFQGFVSVFCFLNSELVRSAIRKRWHRWQDKHSIRARV 391

QY 421 ARAMSIPTSPTRVSPHSHKSTAV 444
DB 392 ARAMSIPTSPTRVSPHSHKSTAV 415

RESULT 10
CRFR1 SHEEP
ID CRFR1 SHEEP STANDARD; PRT; 415 AA.
AC O62772;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Corticotropin releasing factor receptor 1 precursor (CRF-R) (CRF1)
DE (Corticotropin-releasing hormone receptor 1) (CRH-R 1).
GN Name=CRHR1;
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Pituitary;
RX MEDLINE=9907928; PubMed=9863624; DOI=10.1016/S0303-7207(98)00157-9;
RA Myers D.A., Trinh J.V., Myers T.R.;
RT "Structure and function of the ovine type 1 corticotropin releasing
factor receptor (CRF1) and a carboxyl-terminal variant.";
RL Mol. Cell. Endocrinol. 144:21-35(1998).
CC -!- FUNCTION: This is a receptor for corticotropin releasing factor.
CC Shows high-affinity CRF binding. The activity of this receptor is
mediated by G proteins which activate adenylyl cyclase.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- PTM: Carboxyl-terminal Ser or Thr residues may be phosphorylated.
CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 2 family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use as long as its content is in no way modified and this statement is not
removed.
CC -----
CC EMBL; AF054582; AAC08027.1; -; mRNA.
DR InterPro; IPRO03052; CRF1_receptor.
DR InterPro; IPRO03051; CRF_receptor.
DR InterPro; IPRO00832; GPCR secretin.
DR InterPro; IPRO01879; hormn_receptor.
DR PANTHER; PTHR12011:SF16; CRF_receptor; 1.
DR Pfam; PF00002; 7tm_2; 1.
DR Pfam; PF02793; HRM; 1.
DR PRINTS; PR01279; CRFRECEPTOR.
DR PRINTS; PR01280; CRFRECEPTOR1.
DR PRINTS; PR00249; GPCRSECRETIN.
DR SMART; SM00008; Hormr; 1.
DR PROSITE; PS00649; G_PROTEIN_RECEP_F2_1; FALSE_NEG.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; 1.
DR PROSITE; PS02277; G_PROTEIN_RECEP_F2_3; 1.
DR PROSITE; PS50261; G_PROTEIN_RECEP_F2_4; 1.
KW G-protein coupled receptor; Glycoprotein; Phosphorylation; Receptor;
Signal; Transducer; Transmembrane.
FT SIGNAL 1 23 Potential.
FT CHAIN 24 415 Corticotropin releasing factor receptor
1.
FT TOPO_DOM 24 121 Extracellular (Potential).
FT TRANSMEM 122 142 1 (Potential).
FT TOPO_DOM 143 151 Cytoplasmic (Potential).
FT TRANSMEM 152 171 2 (Potential).
FT TOPO_DOM 172 189 Extracellular (Potential).
FT TRANSMEM 190 213 3 (Potential).
FT TOPO_DOM 214 227 Cytoplasmic (Potential).
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FT TRANSMEM 228 249 4 (Potential).
FT TOPO_DOM 250 268 Extracellular (Potential).
FT TRANSMEM 259 291 5 (Potential).
FT TOPO_DOM 292 314 Cytoplasmic (Potential).
FT TRANSMEM 315 334 6 (Potential).
FT TOPO_DOM 335 349 Extracellular (Potential).
FT TRANSMEM 350 369 7 (Potential).
FT TOPO_DOM 370 415 Cytoplasmic (Potential).
FT CARBOHYD 38 38 N-linked (GLCNAC. . .) (Potential).
FT CARBOHYD 45 45 N-linked (GLCNAC. . .) (Potential).
FT CARBOHYD 51 51 N-linked (GLCNAC. . .) (Potential).
FT CARBOHYD 78 78 N-linked (GLCNAC. . .) (Potential).
FT CARBOHYD 90 90 N-linked (GLCNAC. . .) (Potential).
FT CARBOHYD 98 98 N-linked (GLCNAC. . .) (Potential).
FT DISULFID 30 54 By similarity.
FT DISULFID 44 87 By similarity.
FT DISULFID 68 102 By similarity.
SQ SEQUENCE 415 AA; 47559 MW; FA5P652D12B4CDC4 CRC64;

Query Match 87.8%; Score 2086.5; DB 1; Length 415;
Best Local Similarity 88.7%; Pred. No. 9.6e-165;
Matches 394; Conservative 11; Mismatches 10; Indels 29; Gaps 1;

QY 1 MCGHPQLRLVKALLLGLNPVSASLODHCESLSLASNISGLQCNASVDLIGTCWPRSPA 60
DB 1 MGRRPQLRLVKALLLGLNLSISASLODHCESLSLASNISGLQCNASVDLNGTCWPQSPA 60

QY 61 GQLVVRPCAPFFGVRYNTNTNGYRECLANGSWAARVNYSECOILNEEKSKVHYHVAV 120
DB 61 GQLVVRPCLVFFGVRYNTTNGYRVCLANGTWAARVNHSECOELLSEGEKSKAHYHIAV 120

QY 121 IINYLGHCSISLALLVAFVFLRLRPGCTHWGDOADGALEVPAGWPAGPQVRSIRCLR 180
DB 121 IINYLGHCSISLALLVAFVFLRL-----RSIRCLR 151

QY 181 NIHWNLISAFILRNATFVQVLTMSPEVQSNVGCRLVTAAYNYFHTNPFWMGECC 240
DB 152 NIHWNLISAFILRNATFVQVLTMSPEVQSNVGCRLVTAAYNYFHTNPFWMGECC 211

QY 241 YLHTAVLVYSTDLRKWFCICIGWPPPIIIVAWAIGKLYDNEKCFKRPQGVYTDYI 300
DB 212 YLHTAVLVYSTDLRKWFCICIGWPPPIIIVAWAIGKLYDNEKCFKRPQGVYTDYI 271

QY 301 YQGPMLVLLINIFILNIVRIIMTKLRASSTSETIQYKAVKATLVLLPLLGITWMLFF 360
DB 272 YQGPMLVLLINIFILNIVRIIMTKLRASSTSETIQYKAVKATLVLLPLLGITWMLFF 331

QY 361 VNPGEDEVSRVVIYFNSFLESFQGFVSVFYCFNLSEVSAIRKRWHRWQDKHSIRARV 420
DB 332 VNPGEDEVSRVVIYFNSFLESFQGFVSVFYCFNLSEVSAIRKRWHRWQDKHSIRARV 391

QY 421 ARAMSIPTSPRVSFHSIKOSTAV 444
DB 392 ARAMSIPTSPRVSFHSIKOSTAV 415

RESULT 11
ID CRF1 CHICK STANDARD; PRT; 420 AA.
AC Q90812;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Corticotropin releasing factor receptor 1 precursor (CRF-R) (CRF1)
DE (Corticotropin-releasing hormone receptor 1) (CRH-R 1).
GN Name=CRF1;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
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RX MEDLINE=96107136; PubMed=8536612; DOI=10.1210/en.137.1.192;
RA Yu J., Xie L.Y., Abou-Samra A.-B.;
RT "Molecular cloning of a type A chicken corticotropin-releasing factor
RT receptor with high affinity for urotensin I.";
RL Endocrinology 137:192-197(1996).
CC -!- FUNCTION: This is a receptor for corticotropin releasing factor.
CC Shows high-affinity binding for urotensin I. The activity of this
CC receptor is mediated by G proteins which activate adenylyl
CC cyclase.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 2 family.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC EMBL: L41563; AAA96656.1; -; Genomic DNA.
CC Ensembl: ENSGALG00000000371; Gallus_gallus.
CC InterPro: IPR003052; CRF1_receptor.
CC InterPro: IPR003051; CRF_receptor.
CC InterPro: IPR000832; GPCR_secretin.
CC InterPro: IPR001879; hormn_receptor.
CC PANTHER: PTHR12011:SF16; CRF_receptor; 1.
CC Pfam: PF00002; 7tm_2; 1.
CC Pfam: PF02793; HRM; 1.
CC PRINTS; PR01279; CRFRECEPTOR.
CC PRINTS; PR01280; CRFRECEPTOR1.
CC PRINTS; PR00249; GPCRSECRETIN.
CC SMART; SM00008; Hormr; 1.
CC PROSITE; PS00649; G_PROTEIN_RECP_F2_1; 1.
CC PROSITE; PS00650; G_PROTEIN_RECP_F2_2; 1.
CC PROSITE; PS00237; G_PROTEIN_RECP_F2_3; 1.
CC PROSITE; PS0261; G_PROTEIN_RECP_F2_4; 1.
CC G-protein coupled receptor; Glycoprotein; Receptor; Signal;
CC Transducer; Transmembrane.
FT SIGNAL 1 28 Potential.
FT CHAIN 29 420 Corticotropin releasing factor receptor
FT
FT TOPO_DOM 29 126 Extracellular (Potential).
FT TRANSMEM 127 147 1 (Potential).
FT TOPO_DOM 148 156 Cytoplasmic (Potential).
FT TRANSMEM 157 176 2 (Potential).
FT TOPO_DOM 177 194 Extracellular (Potential).
FT TRANSMEM 195 218 3 (Potential).
FT TOPO_DOM 219 232 Cytoplasmic (Potential).
FT TRANSMEM 233 254 4 (Potential).
FT TOPO_DOM 255 273 Extracellular (Potential).
FT TRANSMEM 274 296 5 (Potential).
FT TOPO_DOM 297 319 Cytoplasmic (Potential).
FT TRANSMEM 320 339 6 (Potential).
FT TOPO_DOM 340 354 Extracellular (Potential).
FT TRANSMEM 355 374 7 (Potential).
FT TOPO_DOM 375 420 Cytoplasmic (Potential).
FT CARBOHYD 43 43 N-linked (GLCNAC. . .) (Potential).
FT CARBOHYD 50 50 N-linked (GLCNAC. . .) (Potential).
FT CARBOHYD 83 83 N-linked (GLCNAC. . .) (Potential).
FT CARBOHYD 95 95 N-linked (GLCNAC. . .) (Potential).
FT CARBOHYD 103 103 N-linked (GLCNAC. . .) (Potential).
FT DISULFID 35 59 By similarity.
FT DISULFID 49 92 By similarity.
FT DISULFID 73 107 By similarity.
SQ SEQUENCE 420 AA; 48600 MW; 8C5C92925F62316 CRC64;

Query Match 81.7%; Score 1945; DB 1; Length 420;
Best Local Similarity 82.1%; Pred. No. 5.5e-153;
Matches 366; Conservative 25; Mismatches 23; Indels 32; Gaps 2;

QY 2 GGHPLRLVKALL--LLGLNPVSASLODHCESLSLASNISGLQCNASVDLIGTCWPRS 58
DB 4 GPRPALLLLPLQLQAFLLWDSFVAASIQGYCESLLPTTNHTGQCNASVDLIGTCWPRS 63
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QY 59  PAGQVVRPCPAPFFYGVRYNTNNGYRECLANGSMAARVNYNSQCBILNEEKSKVHYHV 118
DB 64  AVQQLVAPCPBYFYGVRYNTNNGYRECLANGSMAARVNYNSQCBILNEEKSKLHYHI 123
QY 119 AVIINYLGHCISIVALLVAFVFLRLRPGCTHGWDAQDALEVGAPWGPAPQVRRSIRC 178
DB 124 AVIINYLGHCISVGLTLLVAFVFLRML-----RSIRC 154
QY 179 LRNIHNLISAFILRNATFWVQVLTMSDEVHOSNVGWCBLVTAAYNYPHVTNFFWMPGE 238
DB 155 LRNIHNLITAFILRNATFWVQVLTMSDEVHOSNVGWCBLVTAAYNYPHVTNFFWMPGE 214
QY 239 GCYLHTAIVLTSTDLRKLKWMFCIGWGPFFPIIWAIAWAGKLYDNEKCFWGRPGVYTD 298
DB 215 GCYLHTAIVLTSTDLRKLKWMFCIGWGPFFPIIWAIAWAGKLYDNEKCFWGRAGVYTD 274
QY 299 YIYQGMILVLLINFLFNIVRLMTKLRASTTSETIOYRKAVKATLVLLPLLGITYML 358
DB 275 YIYQGMILVLLINFLFNIVRLMTKLRASTTSETIOYRKAVKATLVLLPLLGITYML 334
QY 359 FFYNPGEDEVSRVVFYFNSFLESFQGFVSVFYCFINSEVRSAIRKRWHRWQDKHSIRA 418
DB 335 FFYNPGEDEVSRVVFYFNSFLESFQGFVSVFYCFINSEVRSAIRKRWHRWQDKHSIRA 394
QY 419 RVARMSIPTSPRVSFHSIKQSTAV 444
DB 395 RVARMSIPTSPRVSFHSIKQSSAV 420

RESULT 12
Q98UC2_9TELE
AC Q98UC2_9TELE PRELIMINARY; PRT; 445 AA.
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Corticotropin releasing factor receptor 1.
OS Aneurus nebulosus.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Siluriformes;
OC Ictaluridae; Aneurus.
OX NCBI_TaxID=27778;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21066341; PubMed=11145609; DOI=10.1210/en.142.1.446;
RA Arai M., Asail I.Q., Abou-Samra A.B.;
RT "Characterization of three corticotropin-releasing factor receptors in
RT catfish: a novel third receptor is predominantly expressed in
RT pituitary and urophysis.";
RL Endocrinology 142:446-454(2001).
DR ENBL, AF229359; AAK01068.1; -; mRNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004930; F:G-protein coupled receptor activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin...; IEA.
DR InterPro; IPR003052; CRF_receptor.
DR InterPro; IPR003051; CRF_receptor.
DR InterPro; IPR000832; GPCR_secretin.
DR InterPro; IPR001879; hormn_receptor.
DR Pfam; PF00002; 7tm_2; 1.
DR Pfam; PF02793; HRM_1.
DR PRINTS; PR01279; CRFRECEPTOR.
DR PRINTS; PR01280; CRFRECEPTOR.
DR PRINTS; PR00249; GPCRSECRETIN.
DR SMART; SM00008; Hormr; 1.
DR PROSITE; PS00649; G_PROTEIN_RECP_F2_1; UNKNOWN_1.
DR PROSITE; PS00650; G_PROTEIN_RECP_F2_2; 1.
DR PROSITE; PS0227; G_PROTEIN_RECP_F2_3; 1.
DR PROSITE; PS0261; G_PROTEIN_RECP_F2_4; 1.
DR Receptor.
SQ SEQUENCE 445 AA; 51062 MW; F17DA70BE22BB755 CRC64;

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Query Match 76.3%; Score 1817.5; DB 2; Length 445;
Best Local Similarity 82.9%; Pred. No. 2,3e-142;
Matches 339; Conservative 22; Mismatches 19; Indels 29; Gaps 1;

QY 36 ASNIGSLQCNASVDIIGTCWPRSPAGQLVVRPCPAPFFYGVRYNTNNGYRECLANGSMAA 95
DB 66 SSNATGLFCNISIDIGTCWPRSNAGEIVSRPCPETFLGVRVYNTNNGYRECLANGTMAK 125
QY 96 RVNYSECEIILNEEKSKVHYHVAVIINYLGHCISIVALLVAFVFLRLRPGCTHGWDAQ 155
DB 126 KGNYSQCQBIILNEEKSKLHYHIAVINYLGHCISIGALLVAFILFMR----- 174
QY 156 DGALEVGAPWGPAPQVRRSIRCLRNIIHNLISAFILRNATFWVQVLTMSDEVHOSNVG 215
DB 175 -----RMIRCLRNIIHNLIMAFILRNATFWVQVLTMSDEVHESVNI 216
QY 216 WCLRVTAAYNYPHVTNFFWMPGEVCYLHTAIVLTSTDLRKLKWMFCIGWGPFFPIIWA 275
DB 217 WCLRVTAAYNYPHVTNFFWMPGEVCYLHTAIVLTSTDLRKLKWMFCIGWGPFFPIIWA 276
QY 276 AIGKLYDNEKCFWGRPGVYTDIYQGMILVLLINFLFNIVRLMTKLRASTTSET 335
DB 277 AIGKLYDNEKCFWGRAGVYTDIYQGMILVLLINFLFNIVRLMTKLRASTTSET 336
QY 336 IOYRKAVKATLVLLPLLGITYMLFFVNPGEDEVSRVVFYFNSFLESFQGFVSVFYCF 395
DB 337 IOYRKAVKATLVLLPLLGITYMLFFVNPGEDEVSRVVFYFNSFLESFQGFVSVFYCF 396
QY 396 NSEVRSAIRKRWHRWQDKHSIRARVARMSIPTSPRVSFHSIKQSTAV 444
DB 397 NSEVRSVSRKRWHRWQDKHSIRARVARMSIPTSPRVSFHSIKQSSAV 445

RESULT 13
Q8AWA2_ONCKE
ID Q8AWA2_ONCKE PRELIMINARY; PRT; 430 AA.
AC Q8AWA2;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Corticotropin-releasing factor receptor type 1.
GN Name=crfr1;
OS Oncorhynchus keta (Chum salmon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8018;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Brain;
RA Pohl S., Darlison M.G., Lederis K., Richter D.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ277157; CAC81753.1; -; mRNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004930; F:G-protein coupled receptor activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin...; IEA.
DR InterPro; IPR003052; CRF_receptor.
DR InterPro; IPR003051; CRF_receptor.
DR InterPro; IPR000832; GPCR_secretin.
DR InterPro; IPR001879; hormn_receptor.
DR Pfam; PF00002; 7tm_2; 1.
DR Pfam; PF02793; HRM; 1.
DR PRINTS; PR01279; CRFRECEPTOR.
DR PRINTS; PR01280; CRFRECEPTOR.
DR PRINTS; PR00249; GPCRSECRETIN.
DR SMART; SM00008; Hormr; 1.
DR PROSITE; PS00649; G_PROTEIN_RECP_F2_1; UNKNOWN_1.
DR PROSITE; PS00650; G_PROTEIN_RECP_F2_2; 1.
DR PROSITE; PS0227; G_PROTEIN_RECP_F2_3; 1.
DR PROSITE; PS0261; G_PROTEIN_RECP_F2_4; 1.
DR Receptor.
KW Receptor.

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QY	SEQUENCE	430 AA;	49595 MW;	BCD2CDF36B1281A2 CRC64;
QY	Query Match	75.8%;	Score 1804;	DB 2; Length 430;
DB	Best Local Similarity	74.2%;	Pred. No. 2.9e-141;	
DB	Matches 340;	Conservative	36;	Mismatches 32; Indels 50; Gaps 4;
QY	7	LRLVKALLLGLNPVSASLODHCESLSLASN-----	ISGLQNAS	47
DB	3	LRILPQVLTITWAVVISGTTADLTCDTLLLSLTNLTARTLALWNLTLTPSNVTAGLFCNMS	62	
QY	48	VDLIGTCWPSAGOLVVRPCPAFFYGVRYNTTNGVRECLANGSMAARVNYSECQILN	107	
DB	63	IDPLIGTCWPSAGOLVVRPCPEMFYGVKNTTNNVRECLNSGMAVKNYTCQCEILN	122	
QY	108	EEKSKVHYHVAVIINYLGHCISIVALLVAFVFLRLRPGCTHWGDQADGALEYGAPWSG	167	
DB	123	EXKSKLHYHIAVIINYMGHCISIALALLVAFILFMRL-----	158	
QY	168	APQVRRSIRCLRNI IHWNLLISAPILRNATFWVQVLTMSPEVHQSNGWGRVLTAAVNYF	227	
DB	159	-----RSIRCLRNI IHWNLLITAFILRNATFWVQVLTMPKVNHSNVLWRLVTAAYNYF	212	
QY	228	HVTNFFMFMGEGCVLHTAIVLITYSTDRLRKWMFTICIGWPPPIIIVAWAIGKLYYDNEKC	287	
DB	213	HVTNFFMFMGEGCVLHTAIVLITYSTDRLRKWMFTICIGWPPPIIIVAWAIGKLYYDNEKC	272	
QY	288	WFGKRPQVYTDYIYQGMILVLIINFILFNIIVRLMTKLRASTTSETIOYRKAVKATLV	347	
DB	273	WFGKAGVYTDYIYQGMILVLIINFILFNIIVRLMTKLRASTTSETIOYRKAVKATLV	332	
QY	348	LLPLLGITYMLFFVNP-GEDEVSRVPIYNSFLESFGQFPVSVFYFCFLNSEVRSAIRKR	406	
DB	333	LLPLLGITYMLFFVNPGEDEVAGIVFYNSILESFGQFPVSVFYFCFLNSEVRSVAVRKR	392	
QY	407	WHRWQDKHSIRARVARAMSIPTSPTRVSHSIKOSTAV	444	
DB	393	WHRWQDKHSIRARVARAMSIPTSPTRVSHSIKOSTAV	430	
RESULT 14				
ID	CRFL1_XENLA	STANDARD;	PRT;	415 AA.
AC	O42602;			
DT	15-JUL-1998 (Rel. 36, Created)			
DT	15-JUL-1998 (Rel. 36, Last sequence update)			
DT	10-MAY-2005 (Rel. 47, Last annotation update)			
DE	Corticotropin releasing factor receptor 1 precursor (CRF-R) (CRF1)			
DE	(Corticotropin-releasing hormone receptor 1) (CRH-R 1).			
GN	Name=CRF1;			
OS	Xenopus laevis (African clawed frog).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;			
OC	Xenopodinae; Xenopus; Xenopus.			
OX	NCBI_TaxID=8355;			
RN	[1]			
RC	NUCLEOTIDE SEQUENCE.			
RC	TISSUE=Brain;			
RC	MEDLINE=9745573; PubMed=9326293;			
RA	Dautzenberg F.M., Dietrich K., Falchhaudhuri M.R., Spiess J.;			
RT	"Identification of two corticotropin-releasing factor receptors from			
RT	Xenopus laevis with high ligand selectivity: unusual pharmacology of			
RL	the type 1 receptor."			
RL	J. Neurochem. 69:1649-1649(1997).			
CC	-I- FUNCTION: This is a receptor for corticotropin releasing factor.			
CC	Shows high-affinity binding for urotensin I. The activity of this			
CC	receptor is mediated by G proteins which activate adenylyl cyclase			
CC	(by similarity).			
CC	-I- SUBCELLULAR LOCATION: Integral membrane protein.			
CC	-I- SIMILARITY: Belongs to the G-protein coupled receptor 2 family.			

CC	use as long as its content is in no way modified and this statement is not	
CC	removed.	
CC	EMBL; Y14036; CAAV74363.1; -; mRNA.	
DR	InterPro; IPR003052; CRF1_receptor.	
DR	InterPro; IPR003051; CRF_receptor.	
DR	InterPro; IPR000832; GPCR_secretin.	
DR	InterPro; IPR001879; hormn_receptor.	
DR	PANTHER; PTHR12011:SF16; CRF_receptor; 1.	
DR	Pfam; PF00002; 7tm.2; 1.	
DR	Pfam; PF02793; HRM; 1.	
DR	PRINTS; PR01279; CRFRECEPTOR.	
DR	PRINTS; PR01280; CRFRECEPTOR1.	
DR	PRINTS; PR00249; GPCRSECRETIN.	
DR	SMART; SM00008; Hormr; 1.	
DR	PROSITE; PS00649; G_PROTEIN_RECEP_F2_1; 1.	
DR	PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; 1.	
DR	PROSITE; PS00227; G_PROTEIN_RECEP_F2_3; 1.	
DR	PROSITE; PS00261; G_PROTEIN_RECEP_F2_4; 1.	
KW	G-protein coupled receptor; Glycoprotein; Receptor; Signal;	
KW	Transducer; Transmembrane.	
FT	SIGNAL 1 24 Potential.	
FT	CHAIN 25 415 Corticotropin releasing factor receptor	
FT	1. Extracellular (Potential).	
FT	25 121 Extracellular (Potential).	
FT	TRANSEM 122 142 1 (Potential).	
FT	TOPO_DOM 143 151 Cytoplasmic (Potential).	
FT	TRANSEM 152 171 2 (Potential).	
FT	TOPO_DOM 172 189 Extracellular (Potential).	
FT	TRANSEM 190 213 3 (Potential).	
FT	TOPO_DOM 214 227 Cytoplasmic (Potential).	
FT	TRANSEM 228 249 4 (Potential).	
FT	TOPO_DOM 250 268 Extracellular (Potential).	
FT	TRANSEM 269 291 5 (Potential).	
FT	TOPO_DOM 292 314 Cytoplasmic (Potential).	
FT	TRANSEM 315 334 Extracellular (Potential).	
FT	TOPO_DOM 335 349 6 (Potential).	
FT	TRANSEM 350 369 Extracellular (Potential).	
FT	TOPO_DOM 370 415 Cytoplasmic (Potential).	
FT	CARBOHYD 38 38 N-linked (GLCNAC. . .) (Potential).	
FT	CARBOHYD 45 45 N-linked (GLCNAC. . .) (Potential).	
FT	CARBOHYD 78 78 N-linked (GLCNAC. . .) (Potential).	
FT	CARBOHYD 90 90 N-linked (GLCNAC. . .) (Potential).	
FT	DISULFID 30 54 By similarity.	
FT	DISULFID 44 87 By similarity.	
FT	DISULFID 68 102 By similarity.	
FT	SEQUENCE 415 AA; 47786 MW; 74ED24C17907B74D CRC64;	
QY	Query Match 75.5%; Score 1796.5; DB 1; Length 415;	
QY	Best Local Similarity 75.7%; Pred. No. 1.2e-140;	
QY	Matches 333; Conservative 41; Mismatches 35; Indels 31; Gaps 3;	
QY	5 PQLRLVKALLLLGLNPVSASLDQHCESLSASISGLQCNASVDLIGTCWPSAGOLV 64	
Db	7 PCILLVQ-VIAAGISFALTSLODQ-CETLQHSNFTGLACNASIDMTGTCTWPSAAGOMV 64	
QY	65 VRPCPAFFYGRVYNTNNGVRECLANGSAARVYVSECOILNEEKSKVHYHVAIVNY 124	
Db	65 ARPCPYFHGVQNTVNTGVYRECHLNGSWAGRGDYACQBIILQKQKTKVHYHIAIVNF 124	
QY	125 LGHCISILVALLVAFVLFLRLRPGCTTHGDDQADGALVGPWSPAPFOVRRSIRCLRNIIH 184	
Db	125 LGHSISILCALLVAFILFLRL-----RSIRCLRNIIH 155	
QY	185 WNLISAFILRNATWFFVQVLTMSDEVQSNVGCWRLVTAANYHVTNFFPMWFEGGCYLHT 244	
Db	156 WNLITAFILRNVTWFFVQVLTMSDEVQSNVGCWRLVTAANYHVTNFFPMWFEGGCYLHT 215	
QY	245 AIVLTVSTDLRLKWMFTICIGVGPFPPIIIVAWAIGKLYDNEKCFWGRPGVYTDYIQGP 304	
Db	216 AIVLTVSTDLRLKWMFTICIGVGPFPPIIIVAWAIGKLYDNEKCFWGRPGVYTDYIQGP 275	
QY	305 MIVLVLINFTFLFNIVRLMTKLRASTTSETIOVRKAVKATLVLLPLLGITVYMLFFVNP 364	

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Db 276 VILVLLINPFLNIVRIILMTKLRASSTSETIQYKAVKATVLLPLGLGITYMLFFVTPG 335
QY 365 EDESVRVVFIYFNSPFLSPFGPFVSVFYCPLNSEVRSATKRWHRWQDKHSIRARVAM 424
Db 336 EDBISRIVFIYFNSPFLSPFGPFVSVFYCPLNSEVRSATKRWHRWQDKHSIRARVAM 395
QY 425 SIPTSPTRVSHSIKOSTAV 444
Db 396 SIPTSPTRVSHSIKOSTAV 415

RESULT 15
Q68Y61_RANCA
ID Q68Y61_RANCA PRELIMINARY; PRT; 416 AA.
AC Q68Y61;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DE 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Corticotropin releasing factor receptor type 1.
GN Name=CRFR-1.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana;
OC Aquarana.
OX NCBI_TaxID=8400;
RN [1]
NUCLEOTIDE SEQUENCE.
RA Ito Y., Ogata D., Hasunuma I., Kikuyama S.;
RT "molecular cloning of two corticotropin releasing factor receptors
RT from bullfrog.";
RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB188110; BAD36783.1; -, mRNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR DR GO; GO:0004930; F:G-protein coupled receptor activity; IEA.
DR DR GO; GO:0004872; F:receptor activity; IEA.
DR DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR DR InterPro; IPR003052; CRF1_receptor.
DR DR InterPro; IPR003051; CRF_receptor.
DR DR InterPro; IPR000832; GPCR_secretin.
DR DR InterPro; IPR001879; hormn_receptor.
DR DR Pfam; PF00002; 7tm_2; 1.
DR DR Pfam; PF02793; HRM_1.
DR DR PRINTS; PR01279; CRFRECEPTOR.
DR DR PRINTS; PR01280; CRFRECEPTORL.
DR DR PRINTS; PR00249; GPCRSECRETIN.
DR DR SMART; SM00008; Hormr; 1.
DR DR PROSITE; PS00650; G_PROTEIN_RECP_F2_2; 1.
DR DR PROSITE; PS50227; G_PROTEIN_RECP_F2_3; 1.
DR DR PROSITE; PS50261; G_PROTEIN_RECP_F2_4; 1.
KW Receptor.
SQ SEQUENCE 416 AA; 47798 MW; C7F085BD71916E1B CRC64;

Query Match 75.1%; Score 1789; DB 2; Length 416;
Best Local Similarity 75.9%; Pred No. 4.9e-140;
Matches 337; Conservative 37; Mismatches 32; Indels 38; Gaps 4;

QY 9 LVKALLLLGLNPFVSA-----SLQDQHCESLSLAGNISGLQNASVDLIGTCWPRSPAG 61
Db 3 LSKSPLLLFVQVITAGVSLALTSIQDQ-CENLQSSNITGLACNISIDMIGTCWPRTPAG 61

QY 62 QLVVR-PCPAFFYGVRTNNGYRECLANGSWAARNYISECOILLNEEKSKVHYHVAV 120
Db 62 QLGGHGCPCEPFYFGVQVNTGNYRECHLNGSWAGRGDYTCQCEILKQEKSKVHYHAI 121

QY 121 IINVLGHCSLVALLVAFVLFRLRPGCTHWGDAQDALEVGAPWAGPQVRRSIRCLR 180
Db 122 VINFLGHSISLCALLVAFVLFRL-----RSIRCLR 152

QY 181 NIHWNLISAFILRNATFVVQLTMSGEVHQSNGWCRVLTAANYPHVTNFFWFGEGC 240
Db 153 NIHWNLITAFILRNITFVWQLTLSQEAHDSNVVWCRVLTAHNYFYVTNFFWFGEGC 212
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QY 241 YLHTALVLTYSTDLRKWMFICIGWGPPEPIIWAIGLYYDNEKCMWFGKPGVYTDVI 300
Db 213 YLHTALVLTYSTDLRKWMFICIGWCIPIIWAIGLYYDNEKCMWFGKAGVYTDVI 272
QY 301 YQGPMLVLLINFIPLFNIVRIILMTKLRASSTSETIQYKAVKATVLLPLGLGITYMLFF 360
Db 273 YQGPVILVLLINFIPLFNIVRIILMTKLRASSTSETIQYKAVKATVLLPLGLGITYMLFF 332
QY 361 VNPGEDEVSRVFIYFNSPFLSPFGPFVSVFYCPLNSEVRSATKRWHRWQDKHSIRARV 420
Db 333 VTPGEDEVSRVFIYFNSPFLSPFGPFVSVFYCPLNSEVRSATKRWHRWQDKHSIRARV 392
QY 421 ARAMSIPTSPTRVSHSIKOSTAV 444
Db 393 ARAMSIPTSPTRVSHSIKOSTAV 416

Search completed: March 16, 2006, 17:20:15
Job time : 234 secs
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GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 16, 2006, 17:20:34 ; Search time 47 Seconds  
(without alignments)  
781.021 Million cell updates/sec

Title: US-10-649-193-15  
Perfect score: 2381  
Sequence: 1 MGGHPQLRVKALLLLGLNP.....SIPTSPTRVSFHSIKQSTAV 444

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*

- 1: /cgn2\_6/ptodata/1/iaa/5 COMB.pap.\*
- 2: /cgn2\_6/ptodata/1/iaa/6 COMB.pap.\*
- 3: /cgn2\_6/ptodata/1/iaa/H COMB.pap.\*
- 4: /cgn2\_6/ptodata/1/iaa/PCTUS COMB.pap.\*
- 5: /cgn2\_6/ptodata/1/iaa/RE COMB.pap.\*
- 6: /cgn2\_6/ptodata/1/iaa/backfiles1.pap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2381	100.0	444	2	US-08-482-746-15
2	2381	100.0	444	2	US-09-580-734-15
3	2381	100.0	444	2	US-08-374-009-15
4	2381	100.0	444	2	US-09-191-724-15
5	2381	100.0	444	2	US-09-631-603-11
6	2186.5	91.8	415	1	US-08-110-286A-2
7	2186.5	91.8	415	2	US-08-482-746-2
8	2186.5	91.8	415	2	US-09-580-734-2
9	2186.5	91.8	415	2	US-08-374-009-2
10	2186.5	91.8	415	2	US-09-191-724-2
11	2186.5	91.8	415	2	US-09-799-978-2
12	2186.5	91.8	415	2	US-09-799-978-4
13	2180.5	91.6	415	2	US-09-826-509-483
14	2137.5	89.8	415	2	US-08-482-746-13
15	2137.5	89.8	415	2	US-09-580-734-13
16	2137.5	89.8	415	2	US-08-374-009-13
17	2137.5	89.8	415	2	US-09-191-724-13
18	2137.5	89.8	415	2	US-09-799-978-22
19	2126.5	89.3	415	1	US-08-110-286A-6
20	2126.5	89.3	415	2	US-08-981-189B-10
21	2126.5	89.3	415	2	US-08-482-746-6
22	2126.5	89.3	415	2	US-09-580-734-6
23	2126.5	89.3	415	2	US-08-374-009-6
24	2126.5	89.3	415	2	US-09-191-724-6
25	2126.5	89.3	415	2	US-09-799-978-16
26	2126.5	89.3	415	2	US-09-799-978-40
27	2092.5	87.9	401	2	US-09-799-978-8

28	2086.5	87.6	415	2	US-09-799-978-28	Sequence 28, Appl
29	1945	81.7	420	2	US-09-799-978-42	Sequence 42, Appl
30	1925.5	80.9	375	2	US-09-799-978-6	Sequence 6, Appl
31	1817.5	76.3	445	2	US-09-799-978-34	Sequence 34, Appl
32	1796.5	75.5	415	2	US-09-799-978-30	Sequence 30, Appl
33	1741.5	73.1	428	2	US-09-799-978-36	Sequence 36, Appl
34	1574.5	66.1	438	2	US-09-799-978-12	Sequence 12, Appl
35	1562	65.6	431	2	US-08-981-189B-13	Sequence 13, Appl
36	1562	65.6	431	2	US-09-881-401-2	Sequence 2, Appl
37	1561	65.6	405	2	US-09-799-978-38	Sequence 38, Appl
38	1556	65.4	431	1	US-08-381-433A-2	Sequence 4, Appl
39	1550.5	65.1	411	1	US-08-381-433A-4	Sequence 12, Appl
40	1550.5	65.1	411	2	US-08-981-189B-12	Sequence 18, Appl
41	1550.5	65.1	411	2	US-09-799-978-18	Sequence 4, Appl
42	1550.5	65.1	411	2	US-09-881-401-4	Sequence 12, Appl
43	1549.5	65.1	411	2	US-09-631-603-12	Sequence 20, Appl
44	1549	65.1	431	2	US-09-799-978-20	Sequence 14, Appl
45	1547.5	65.0	397	2	US-09-799-978-14	

ALIGNMENTS

RESULT 1  
US-08-482-746-15  
; Sequence 15, Application US/08482746B  
; Patent No. 6399315  
; GENERAL INFORMATION:  
; APPLICANT: Perrin, Marilyn H.  
; APPLICANT: Chen, Ruoping  
; APPLICANT: Lewis, Kathy A.  
; APPLICANT: Vale Jr., Wylie W.  
; APPLICANT: Donaldson, Cynthia J.  
; APPLICANT: Sawchenko, Paul  
; TITLE OF INVENTION: Cloning and Recombinant Production of  
; FILE REFERENCE: P41-90002  
; CURRENT APPLICATION NUMBER: US/08/482,746B  
; CURRENT FILING DATE: 1995-06-07  
; EARLIER APPLICATION NUMBER: US 08/374,009  
; EARLIER FILING DATE: 1995-01-17  
; EARLIER APPLICATION NUMBER: US 08/353,537  
; EARLIER FILING DATE: 1994-12-09  
; EARLIER APPLICATION NUMBER: PCT/US94/05908  
; EARLIER FILING DATE: 1994-05-25  
; EARLIER APPLICATION NUMBER: US 08/110,286  
; EARLIER FILING DATE: 1993-08-23  
; EARLIER APPLICATION NUMBER: US 08/079,320  
; EARLIER FILING DATE: 1993-06-18  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 15  
; LENGTH: 444  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-08-482-746-15

Query Match	100.0%;	Score 2381;	DB 2;	Length 444;
Best Local Similarity	100.0%;	Pred. No. 1.2e-232;		
Matches 444;	Conservative	0;	Mismatches	0; Gaps 0;
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Db	1	MGGHPQLRVKALLLLGLNPVSASLQDQCESLSLASNISGLQCNASVDLIGTCWPRSPA	60	
Qy	61	GQLVWRPCPAFFVGYRYNTTNGYRECLANGSWAARNYSECOILNEEKKSVHYHAV	120	
Db	61	GQLVWRPCPAFFVGYRYNTTNGYRECLANGSWAARNYSECOILNEEKKSVHYHAV	120	
Qy	121	IINVLGHICISLVALLVAFVLFLRLPCTHWGDAQLEVGAPWSGAPFQVRRSIRCLR	180	
Db	121	IINVLGHICISLVALLVAFVLFLRLPCTHWGDAQLEVGAPWSGAPFQVRRSIRCLR	180	

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DB 181 NIIHWNLSAFILRNATFWVQLTMSPEVHQSNGWCRLVTAAYNFHVHTNPFWMFGECC 240
QY 241 YLHTAIVLTSTDRLRKWMFICIGWGVPPPIIVAMAIGKLYYDNEKCFGKRPVYTDYI 300
DB 241 YLHTAIVLTSTDRLRKWMFICIGWGVPPPIIVAMAIGKLYYDNEKCFGKRPVYTDYI 300
QY 301 YQGPMLVLVLLINFIPLFNIVRIILMTKLRASTTSETIOYRKAVKATVLLPLLGITTYMLPF 360
DB 301 YQGPMLVLVLLINFIPLFNIVRIILMTKLRASTTSETIOYRKAVKATVLLPLLGITTYMLPF 360
QY 361 VNPGEDEVSRVVIYFNSFLESFQGFVSFVFCFLNSEVSAIRKRWHRQDKHSIRARV 420
DB 361 VNPGEDEVSRVVIYFNSFLESFQGFVSFVFCFLNSEVSAIRKRWHRQDKHSIRARV 420
QY 421 ARAMSIPTSPTRVSVFHSIKOSTAV 444
DB 421 ARAMSIPTSPTRVSVFHSIKOSTAV 444
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## RESULT 2

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US-09-580-734-15
; Sequence 15, Application US/09580734
; Patent No. 6482608
; GENERAL INFORMATION:
; APPLICANT: Perrin, Marilyn H.
; APPLICANT: Chen, Ruoping
; APPLICANT: Lewis, Kathy A.
; APPLICANT: Vale Jr., Wylie W.
; APPLICANT: Donaldson, Cynthia J.
; APPLICANT: Sawchenko, Paul
; TITLE OF INVENTION: Cloning and Recombinant Production of
; FILE OF INVENTION: CRF Receptor(s)
; FILE REFERENCE: Salk1748
; CURRENT APPLICATION NUMBER: US/09/580,734
; CURRENT FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 09/191,724
; PRIOR FILING DATE: 1998-11-12
; PRIOR APPLICATION NUMBER: US 08/374,009
; PRIOR FILING DATE: 1995-01-17
; PRIOR APPLICATION NUMBER: US 08/353,537
; PRIOR FILING DATE: 1994-12-09
; PRIOR APPLICATION NUMBER: PCT/US94/05908
; PRIOR FILING DATE: 1993-05-25
; PRIOR APPLICATION NUMBER: US 08/110,286
; PRIOR FILING DATE: 1993-08-23
; PRIOR APPLICATION NUMBER: US 08/079,320
; PRIOR FILING DATE: 1993-06-18
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 15
; LENGTH: 444
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-580-734-15
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Query Match 100.0%; Score 2381; DB 2; Length 444;
Best Local Similarity 100.0%; Pred. No. 1.2e-232;
Matches 444; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGGHPQLRLVKALLLGLNPNVSASLQDQHCESLSLASNISGLQCNASVDLIGTCWPRSPA 60
DB 1 MGGHPQLRLVKALLLGLNPNVSASLQDQHCESLSLASNISGLQCNASVDLIGTCWPRSPA 60
QY 61 GQLVVRPCPAFFVGVRYNTTNGYRECLANGSWAARVNYSECOIINEEKSKVHYHVAV 120
DB 61 GQLVVRPCPAFFVGVRYNTTNGYRECLANGSWAARVNYSECOIINEEKSKVHYHVAV 120
QY 121 IINYLGHCSLVALLVAVFLRLRPGCTHWGDQADGALEVGAPWSGAPQVRRSIRCLR 180
DB 121 IINYLGHCSLVALLVAVFLRLRPGCTHWGDQADGALEVGAPWSGAPQVRRSIRCLR 180
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DB 181 NIIHWNLSAFILRNATFWVQLTMSPEVHQSNGWCRLVTAAYNFHVHTNPFWMFGECC 240
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DB 241 YLHTAIVLTSTDRLRKWMFICIGWGVPPPIIVAMAIGKLYYDNEKCFGKRPVYTDYI 300
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DB 301 YQGPMLVLVLLINFIPLFNIVRIILMTKLRASTTSETIOYRKAVKATVLLPLLGITTYMLPF 360
QY 361 VNPGEDEVSRVVIYFNSFLESFQGFVSFVFCFLNSEVSAIRKRWHRQDKHSIRARV 420
DB 361 VNPGEDEVSRVVIYFNSFLESFQGFVSFVFCFLNSEVSAIRKRWHRQDKHSIRARV 420
QY 421 ARAMSIPTSPTRVSVFHSIKOSTAV 444
DB 421 ARAMSIPTSPTRVSVFHSIKOSTAV 444
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## RESULT 3

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US-08-374-009-15
; Sequence 15, Application US/08374009A
; Patent No. 6495343
; GENERAL INFORMATION:
; APPLICANT: Perrin, Marilyn H.
; APPLICANT: Chen, Ruoping
; APPLICANT: Lewis, Kathy A.
; APPLICANT: Vale Jr., Wylie W.
; APPLICANT: Donaldson, Cynthia J.
; APPLICANT: Sawchenko, Paul
; TITLE OF INVENTION: Cloning and Recombinant Production of
; FILE OF INVENTION: CRF Receptor(s)
; FILE REFERENCE: P41 9886
; CURRENT APPLICATION NUMBER: US/08/374,009A
; CURRENT FILING DATE: 1995-01-17
; PRIOR APPLICATION NUMBER: US 08/353,537
; PRIOR FILING DATE: 1994-12-09
; PRIOR APPLICATION NUMBER: US 08/079,320
; PRIOR FILING DATE: 1993-06-18
; PRIOR APPLICATION NUMBER: US 08/110,286
; PRIOR FILING DATE: 1993-08-23
; PRIOR APPLICATION NUMBER: PCT/US94/05908
; PRIOR FILING DATE: 1994-05-25
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 15
; LENGTH: 444
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-374-009-15
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Query Match 100.0%; Score 2381; DB 2; Length 444;
Best Local Similarity 100.0%; Pred. No. 1.2e-232;
Matches 444; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MGGHPQLRLVKALLLGLNPNVSASLQDQHCESLSLASNISGLQCNASVDLIGTCWPRSPA 60
QY 61 GQLVVRPCPAFFVGVRYNTTNGYRECLANGSWAARVNYSECOIINEEKSKVHYHVAV 120
DB 61 GQLVVRPCPAFFVGVRYNTTNGYRECLANGSWAARVNYSECOIINEEKSKVHYHVAV 120
QY 121 IINYLGHCSLVALLVAVFLRLRPGCTHWGDQADGALEVGAPWSGAPQVRRSIRCLR 180
DB 121 IINYLGHCSLVALLVAVFLRLRPGCTHWGDQADGALEVGAPWSGAPQVRRSIRCLR 180
QY 181 NIIHWNLSAFILRNATFWVQLTMSPEVHQSNGWCRLVTAAYNFHVHTNPFWMFGECC 240
DB 181 NIIHWNLSAFILRNATFWVQLTMSPEVHQSNGWCRLVTAAYNFHVHTNPFWMFGECC 240
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RESULT 5
US-09-631-603-11
; Sequence 11, Application US/09631603
; Patent No. 6733990
; GENERAL INFORMATION:
; APPLICANT: Hodge, Martin R.
; APPLICANT: Lloyd, Clare
; APPLICANT: Weich, Nadine
; TITLE OF INVENTION: 1571, A No. 6733990el GPCR-like Molecule of the
; TITLE OF INVENTION: Secretin-Like Family and Uses Thereof
; FILE REFERENCE: 5800-48A
; CURRENT APPLICATION NUMBER: US/09/631,603
; CURRENT FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 09/515,781
; PRIOR FILING DATE: 2000-02-29
; PRIOR APPLICATION NUMBER: 60/146,916
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 11
; LENGTH: 444
; TYPE: PRT

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US-09-631-603-11
; Sequence 11, Application US/09631603
; Patent No. 673390
; GENERAL INFORMATION:
; APPLICANT: Hodge, Martin R.
; APPLICANT: Lloyd, Clare
; APPLICANT: Weich, Nadine
; TITLE OF INVENTION: 15571, A No. 6733990el GPCR-like Molecule of the
; SECRETIN-LIKE FAMILY AND USES THEREOF
; FILE REFERENCE: 5800-48A
; CURRENT APPLICATION NUMBER: US/09/631,603
; CURRENT FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 09/515,781
; PRIOR FILING DATE: 2000-02-29
; PRIOR APPLICATION NUMBER: 60/146,916
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 11
; LENGTH: 444
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-631-603-11

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	Dd	1	MGGHPQLRVKALLIGLGNPNVSLQDQHCHESLSASNISSLQCNASVDLTGTCPWSPA	60

Db 61 GQLVREPCPAFFGVRYNTTNGVRECLANGSWAARVNYSECQILNEKKSKVHYHVAV 120

Qy 121 IINVLGHCIISLVALLVAFVLFLRLPGCTHWGQDQDGALEFVGAPWSGAPFVRRSIRCLR 180

Q7	241	YLHTAIVLTSTDRLRKWMFCICGWPPPIIVAWAIGKLYYDNEKWFGRKPGVYTDYI	300
D6	241	YLHTAIVLTSTDRLRKWMFCICGWPPPIIVAWAIGKLYYDNEKWFGRKPGVYTDYI	300

	Qy	Db
361	VNPGDEVSRWFTYFNSPLESFGGFFVSFYCFYNSEVSASRKRWHRWQDKHSIRARV	420
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QV 421 ARAMSIPTSPTRVSFHSIKQSTAV 444

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Db      421 ARAMSIPTSPTRVSHSIKQSTAV 444
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US-08-110-286A-2
; Sequence 2, Application US/08110286A
; Patent No. 5728545
; GENERAL INFORMATION:
; APPLICANT: Perrin, Marilyn H.
; APPLICANT: Chen, Ruoping
; APPLICANT: Lewis, Kathy A.
; APPLICANT: Vale Jr., Wylie W.
; APPLICANT: Donaldson, Cynthia J.
; TITLE OF INVENTION: CLONING AND RECOMBINANT PRODUCTION OF
; TITLE OF INVENTION: CRF RECEPTOR(S)
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark
; STREET: 444 South Flower Street, Suite 2000
; CITY: Los Angeles
; STATE: CA
; COUNTRY: USA
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patencin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/110,286A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/079,320
; FILING DATE: 18-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Reiter, Stephen E.
; REGISTRATION NUMBER: 31,192
; REFERENCE/DOCKET NUMBER: P41 9439
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-546-4737
; TELEFAX: 619-546-9392
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 415 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-110-286A-2

Query Match          91.8%; Score 2186.5; DB 1; Length 415;
Best Local Similarity 93.5%; Pred. No. 5.7e-213;
Matches 415; Conservative 0; Mismatches 0; Indels 29; Gaps 1;

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Db      1 MGGHPQLRLVKALLLGLNPVSASLQDQHCESLSLASNISGLQCNASVDLIGTCWPRSPA 60
QY      61 GQLVVRPCPAFFYGVRYNTTNGYRECLANGSWAARVNYSECQEIINEEKKSKVHYHVAV 120
Db      61 GQLVVRPCPAFFYGVRYNTTNGYRECLANGSWAARVNYSECQEIINEEKKSKVHYHVAV 120
QY      121 IINYLGHCSLSVALLVAVFLRLRPGCTHWGDAQDGALEVGAPWPGAPFQVRRSRICLR 180
Db      121 IINYLGHCSLSVALLVAVFLRLRPGCTHWGDAQDGALEVGAPWPGAPFQVRRSRICLR 180
QY      181 NIHNWNLISAFILRNATWFFVQLTMSPEVHQSNVGCRLVTAAYNFVHTNPFWMFGECC 240
Db      152 NIHNWNLISAFILRNATWFFVQLTMSPEVHQSNVGCRLVTAAYNFVHTNPFWMFGECC 211
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Db      241 YLHTAIVLTYSTDRLRKWMFICIGWGVPPPIIVAMAIGKLYYDNEKCMWFGKRGPGVYTDYI 300

Db      421 ARAMSIPTSPTRVSHSIKQSTAV 444
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RESULT 7
US-08-482-746-2
; Sequence 2, Application US/08482746B
; Patent No. 6399315
; GENERAL INFORMATION:
; APPLICANT: Perrin, Marilyn H.
; APPLICANT: Chen, Ruoping
; APPLICANT: Lewis, Kathy A.
; APPLICANT: Vale Jr., Wylie W.
; APPLICANT: Donaldson, Cynthia J.
; APPLICANT: Sawchenko, Paul
; TITLE OF INVENTION: Cloning and Recombinant Production of
; TITLE OF INVENTION: CRF Receptor(s)
; FILE REFERENCE: P41-90002
; CURRENT APPLICATION NUMBER: US/08/482,746B
; CURRENT FILING DATE: 1995-06-07
; EARLIER APPLICATION NUMBER: US 08/374,009
; EARLIER FILING DATE: 1995-01-17
; EARLIER APPLICATION NUMBER: US 08/353,537
; EARLIER FILING DATE: 1994-12-09
; EARLIER APPLICATION NUMBER: PCT/US94/05908
; EARLIER FILING DATE: 1994-05-25
; EARLIER APPLICATION NUMBER: US 08/110,286
; EARLIER FILING DATE: 1993-08-23
; EARLIER APPLICATION NUMBER: US 08/079,320
; EARLIER FILING DATE: 1993-06-18
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 415
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-482-746-2

Query Match          91.8%; Score 2186.5; DB 2; Length 415;
Best Local Similarity 93.5%; Pred. No. 5.7e-213;
Matches 415; Conservative 0; Mismatches 0; Indels 29; Gaps 1;

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Db      1 MGGHPQLRLVKALLLGLNPVSASLQDQHCESLSLASNISGLQCNASVDLIGTCWPRSPA 60
QY      61 GQLVVRPCPAFFYGVRYNTTNGYRECLANGSWAARVNYSECQEIINEEKKSKVHYHVAV 120
Db      61 GQLVVRPCPAFFYGVRYNTTNGYRECLANGSWAARVNYSECQEIINEEKKSKVHYHVAV 120
QY      121 IINYLGHCSLSVALLVAVFLRLRPGCTHWGDAQDGALEVGAPWPGAPFQVRRSRICLR 180
Db      121 IINYLGHCSLSVALLVAVFLRLRPGCTHWGDAQDGALEVGAPWPGAPFQVRRSRICLR 180
QY      181 NIHNWNLISAFILRNATWFFVQLTMSPEVHQSNVGCRLVTAAYNFVHTNPFWMFGECC 240
Db      152 NIHNWNLISAFILRNATWFFVQLTMSPEVHQSNVGCRLVTAAYNFVHTNPFWMFGECC 211
QY      241 YLHTAIVLTYSTDRLRKWMFICIGWGVPPPIIVAMAIGKLYYDNEKCMWFGKRGPGVYTDYI 300
Db      241 YLHTAIVLTYSTDRLRKWMFICIGWGVPPPIIVAMAIGKLYYDNEKCMWFGKRGPGVYTDYI 300
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QY 301 YQGPMLVLLINFIPLFNIVIRILMTKLRASSTTSETIOYKAVKATVLLPLLGITTYMLFF 360  
DB 272 YQGPMLVLLINFIPLFNIVIRILMTKLRASSTTSETIOYKAVKATVLLPLLGITTYMLFF 331  
QY 361 VNPGEDEVSRVFIYFNSEFLSFQGFVSVFYCFNLSEVRSARKEHWRQDKHSIRARV 420  
DB 332 VNPGEDEVSRVFIYFNSEFLSFQGFVSVFYCFNLSEVRSARKEHWRQDKHSIRARV 391  
QY 421 ARAMSIPTSPTRVSPHSHIKQSTAV 444  
DB 392 ARAMSIPTSPTRVSPHSHIKQSTAV 415

## RESULT 8

US-09-580-734-2  
; Sequence 2, Application US/09580734  
; Patent No. 6482608  
; GENERAL INFORMATION:  
; APPLICANT: Perrin, Marilyn H.  
; APPLICANT: Chen, Ruoping  
; APPLICANT: Lewis, Kathy A.  
; APPLICANT: Vale Jr., Wylie W.  
; APPLICANT: Donaldson, Cynthia J.  
; APPLICANT: Sawchenko, Paul  
; TITLE OF INVENTION: Cloning and Recombinant Production of  
; TITLE OF INVENTION: CRF Receptor(s)  
; FILE REFERENCE: Salk1748  
; CURRENT APPLICATION NUMBER: US/09/580,734  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: 09/191,724  
; PRIOR FILING DATE: 1998-11-12  
; PRIOR APPLICATION NUMBER: US 08/374,009  
; PRIOR FILING DATE: 1995-01-17  
; PRIOR APPLICATION NUMBER: US 08/353,537  
; PRIOR FILING DATE: 1994-12-09  
; PRIOR APPLICATION NUMBER: PCT/US94/05908  
; PRIOR FILING DATE: 1993-05-25  
; PRIOR APPLICATION NUMBER: US 08/110,286  
; PRIOR FILING DATE: 1993-08-23  
; PRIOR APPLICATION NUMBER: US 08/079,320  
; PRIOR FILING DATE: 1993-06-18  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 2  
; LENGTH: 415  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-580-734-2

Query Match 91.8%; Score 2186.5; DB 2; Length 415;  
Best Local Similarity 93.5%; Pred. No. 5.7e-213;  
Matches 415; Conservative 0; Mismatches 0; Indels 29; Gaps 1;  
QY 1 MGHGPQLRLVKALLLLGLNPNVSASLQDQHCESLSLASNISGLQCNASVDLIGTCWPRSPA 60  
DB 1 MGHGPQLRLVKALLLLGLNPNVSASLQDQHCESLSLASNISGLQCNASVDLIGTCWPRSPA 60  
QY 61 GOLVVRPCPAFFYGVRYNTTNGYRECLANGSNAARVNYSECOEILNEEKSKVHHVAV 120  
DB 61 GOLVVRPCPAFFYGVRYNTTNGYRECLANGSNAARVNYSECOEILNEEKSKVHHVAV 120  
QY 121 IINYLGHCHISLVALLVAFVFLRLRPGCTHWGDAQDGALEVGAPWPGAPQVRRSIRCLR 180  
DB 121 IINYLGHCHISLVALLVAFVFLRLRPGCTHWGDAQDGALEVGAPWPGAPQVRRSIRCLR 151  
QY 181 NIHNWNLISAFILRNATVFWVQLTMSPEVHQSNVGCRLVTAAYNYFHVNTFFWFMFEGC 240  
DB 152 NIHNWNLISAFILRNATVFWVQLTMSPEVHQSNVGCRLVTAAYNYFHVNTFFWFMFEGC 211  
QY 241 YLHTAIVLTSTDRLRKWMFICIGWGPFPPIIVAWAIGKLYYDNEKVCWFGKRGVYTDYI 300  
DB 212 YLHTAIVLTSTDRLRKWMFICIGWGPFPPIIVAWAIGKLYYDNEKVCWFGKRGVYTDYI 271

QY 301 YQGPMLVLLINFIPLFNIVIRILMTKLRASSTTSETIOYKAVKATVLLPLLGITTYMLFF 360  
DB 272 YQGPMLVLLINFIPLFNIVIRILMTKLRASSTTSETIOYKAVKATVLLPLLGITTYMLFF 331  
QY 361 VNPGEDEVSRVFIYFNSEFLSFQGFVSVFYCFNLSEVRSARKEHWRQDKHSIRARV 420  
DB 332 VNPGEDEVSRVFIYFNSEFLSFQGFVSVFYCFNLSEVRSARKEHWRQDKHSIRARV 391  
QY 421 ARAMSIPTSPTRVSPHSHIKQSTAV 444  
DB 392 ARAMSIPTSPTRVSPHSHIKQSTAV 415

## RESULT 9

US-08-374-009-2  
; Sequence 2, Application US/08374009A  
; Patent No. 6495343  
; GENERAL INFORMATION:  
; APPLICANT: Perrin, Marilyn H.  
; APPLICANT: Chen, Ruoping  
; APPLICANT: Lewis, Kathy A.  
; APPLICANT: Vale Jr., Wylie W.  
; APPLICANT: Donaldson, Cynthia J.  
; APPLICANT: Sawchenko, Paul  
; TITLE OF INVENTION: Cloning and Recombinant Production of  
; TITLE OF INVENTION: CRF Receptor(s)  
; FILE REFERENCE: P41 9886  
; CURRENT APPLICATION NUMBER: US/08/374,009A  
; PRIOR FILING DATE: 1995-01-17  
; PRIOR APPLICATION NUMBER: US 08/353,537  
; PRIOR FILING DATE: 1994-12-09  
; PRIOR APPLICATION NUMBER: US 08/079,320  
; PRIOR FILING DATE: 1993-06-18  
; PRIOR APPLICATION NUMBER: US 08/110,286  
; PRIOR FILING DATE: 1993-08-23  
; PRIOR APPLICATION NUMBER: PCT/US94/05908  
; PRIOR FILING DATE: 1994-05-25  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 2  
; LENGTH: 415  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-08-374-009-2

Query Match 91.8%; Score 2186.5; DB 2; Length 415;  
Best Local Similarity 93.5%; Pred. No. 5.7e-213;  
Matches 415; Conservative 0; Mismatches 0; Indels 29; Gaps 1;

QY 1 MGHGPQLRLVKALLLLGLNPNVSASLQDQHCESLSLASNISGLQCNASVDLIGTCWPRSPA 60  
DB 1 MGHGPQLRLVKALLLLGLNPNVSASLQDQHCESLSLASNISGLQCNASVDLIGTCWPRSPA 60  
QY 61 GOLVVRPCPAFFYGVRYNTTNGYRECLANGSNAARVNYSECOEILNEEKSKVHHVAV 120  
DB 61 GOLVVRPCPAFFYGVRYNTTNGYRECLANGSNAARVNYSECOEILNEEKSKVHHVAV 120  
QY 121 IINYLGHCHISLVALLVAFVFLRLRPGCTHWGDAQDGALEVGAPWPGAPQVRRSIRCLR 180  
DB 121 IINYLGHCHISLVALLVAFVFLRLRPGCTHWGDAQDGALEVGAPWPGAPQVRRSIRCLR 151  
QY 181 NIHNWNLISAFILRNATVFWVQLTMSPEVHQSNVGCRLVTAAYNYFHVNTFFWFMFEGC 240  
DB 152 NIHNWNLISAFILRNATVFWVQLTMSPEVHQSNVGCRLVTAAYNYFHVNTFFWFMFEGC 211  
QY 241 YLHTAIVLTSTDRLRKWMFICIGWGPFPPIIVAWAIGKLYYDNEKVCWFGKRGVYTDYI 300  
DB 212 YLHTAIVLTSTDRLRKWMFICIGWGPFPPIIVAWAIGKLYYDNEKVCWFGKRGVYTDYI 271  
QY 301 YQGPMLVLLINFIPLFNIVIRILMTKLRASSTTSETIOYKAVKATVLLPLLGITTYMLFF 360  
DB 272 YQGPMLVLLINFIPLFNIVIRILMTKLRASSTTSETIOYKAVKATVLLPLLGITTYMLFF 331

Qy	361	VNPGDEVRVVFIYFNSEVFLSPQGFVSVFYCFLNGSEVSAIKRWHRWQDKHSIRARV	420
Db	332	VNPGDEVRVVFIYFNSEVFLSPQGFVSVFYCFLNGSEVSAIKRWHRWQDKHSIRARV	391
Qy	421	ARAMSIPTSPTRVSFHSIKQSTAV	444
Db	392	ARAMSIPTSPTRVSFHSIKQSTAV	415

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RESULT 10
US-09-191-724-2
; Sequence 2, Application US/09191724
; Patent No. 6638905
; GENERAL INFORMATION:
; APPLICANT: Perrin, Marilyn H.
; APPLICANT: Lewis, Kathy A.
; APPLICANT: Vale Jr., Wylie W.
; APPLICANT: Donaldson, Cynthia J.
; APPLICANT: Sawchenko, Paul
; TITLE OF INVENTION: Cloning and Recombinant Production of
; TITLE OF INVENTION: CRF Receptor(s)
; FILE REFERENCE: Salk1748
; CURRENT APPLICATION NUMBER: US/09/191,724
; CURRENT FILING DATE: 1998-11-12
; EARLIER APPLICATION NUMBER: US 08/374,009
; EARLIER FILING DATE: 1995-01-17
; EARLIER APPLICATION NUMBER: US 08/353,537
; EARLIER FILING DATE: 1994-12-09
; EARLIER APPLICATION NUMBER: PCT/US94/05908
; EARLIER FILING DATE: 1993-05-25
; EARLIER APPLICATION NUMBER: US 08/110,286
; EARLIER FILING DATE: 1993-08-23
; EARLIER APPLICATION NUMBER: US 08/079,320
; EARLIER FILING DATE: 1993-06-18
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 415
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-191-724-2

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Query Match	91.8%;	Score 2186.5;	DB 2;	Length 415;
Best Local Similarity	93.5%;	Pred. No. 5.7e-213;		
Matches 415;	Conservative 0;	Mismatches 0;	Indels 29;	Gaps 1;

  

Qy	1	MGGHPQLRLVKALLLGLNPVSASLSAQDHCHESLSLASNISGLQCNASVDLIGTCWPRSPA	60
Db	1	MGGHPQLRLVKALLLGLNPVSASLSAQDHCHESLSLASNISGLQCNASVDLIGTCWPRSPA	60
Qy	61	GQLVVRPCPAFFYGVRRYNTTNGVRECLANGSMAARVNYSECQILNEEKSKKVHYHVAV	120
Db	61	GQLVVRPCPAFFYGVRRYNTTNGVRECLANGSMAARVNYSECQILNEEKSKKVHYHVAV	120
Qy	121	IINYLGHCISLIVALLVAVFLRLRPGCTHWGDQADGALVGAPWSGAPFQVRRESIRCLR	180
Db	121	IINYLGHCISLIVALLVAVFLRL-----RSIRCLR	151
Qy	181	NIHWNLIISAFILRNATWFFVQLTMSPEVHQSNVGMWCLRVTAAYNYFHVTFNFMFGECC	240
Db	152	NIHWNLIISAFILRNATWFFVQLTMSPEVHQSNVGMWCLRVTAAYNYFHVTFNFMFGECC	211
Qy	241	YLHTAIVLVTSTDBLRKMMFICIGWGPFPPIIVAWAIGKLYYDNKCFWPKRPGVYTDYI	300
Db	212	YLHTAIVLVTSTDBLRKMMFICIGWGPFPPIIVAWAIGKLYYDNKCFWPKRPGVYTDYI	271
Qy	301	YQGPMLIVLLINFLFNIVRILMTKLRASTTSETIOVRKAVKATVLLPLLGITYMLFF	360
Db	272	YQGPMLIVLLINFLFNIVRILMTKLRASTTSETIOVRKAVKATVLLPLLGITYMLFF	331
Qy	361	VNPGQEDSVSRVVFYTFNPSFLSFQGFVSPVFCFLNSEVRSAIRKRWHRMWDKHSIRARV	420

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Dbb      332 VNPGEDEVSRVVFIYFNSFLIESFGGFVSVFYCFLNSEVRSAIRKRWHRWQDKHSIRARV    3991
          Qy       421 ARAMSIFTSPTRVSFHSHIKOSTAV   444
                |||||
Ddb      392 ARAMSIFTSPTRVSFHSHIKOSTAV   415
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RESULT 11  
US-09-799-978-2  
; Sequence 2, Application US/097999578  
; Patent No. 6670140  
; GENERAL INFORMATION:  
; APPLICANT: The Procter & Gamble Company  
; APPLICANT: Isfort, Robert  
; APPLICANT: Sheldon, Russell  
; TITLE OF INVENTION: Methods for Identifying Compounds for Regulating Musc...  
; TITLE OF INVENTION: Function Using Corticotropin Releasing Factor Receptor...  
; FILE REFERENCE: 8448  
; CURRENT APPLICATION NUMBER: US/09/799,978  
; CURRENT FILING DATE: 2001-03-06  
; NUMBER OF SEQ ID NOS: 44  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 2  
; LENGTH: 415  
; TYPE: PRT  
; ORGANISM: homo sapiens  
US-09-799-978-2

Query Match	91.8%	Score 2186.5	DB 2	Length 415
Best Local Similarity	93.5%	Pred. No. 5.7e-213		
Matches 415	Conservative 0	Mismatches 0	Indels 29	Gaps 1
Qy 1	MGGHPQLRLVKALLLGINPVASLSLOQHCHESLSLASNISGLQCNASVDLIGTCHWRSPA	60		
Db 1	MGGHPQLRLVKALLLGINPVASLSLOQHCHESLSLASNISGLQCNASVDLIGTCHWRSPA	60		
Qy 61	GQLVVRPCPAFFYGVRRYNTTNGVRECLANGSWAARVNNYSECQETLNEEKSKVHHYHAV	120		
Db 61	GQLVVRPCPAFFYGVRRYNTTNGVRECLANGSWAARVNNYSECQETLNEEKSKVHHYHAV	120		
Qy 121	IINYLGHCISLVALLVAFVFLRLRPGCTHMGDQADGALGVGAPMSGAPFQVRRSIRCLR	180		
Db 121	IINYLGHCISLVALLVAFVFLRL-----RSLRCLR	151		
Qy 181	NITHWNLISAFILBNATWVQVLTMSPEVHOSNVGWCRLVTAAYNYFVYTNPFPMWFGEGC	240		
Db 152	NITHWNLISAFILBNATWVQVLTMSPEVHOSNVGWCRLVTAAYNYFVYTNPFPMWFGEGC	211		
Qy 241	YLHTAIVLVTSTDRLRKWMFTICIGWGVPFPIIIVAWAIGKLYYDNKCFGKRPGVYTDVI	300		
Db 212	YLHTAIVLVTSTDRLRKWMFTICIGWGVPFPIIIVAWAIGKLYYDNKCFGKRPGVYTDVI	271		
Qy 301	YQGPMLVLVLINFIPLFNIRVILMTKLRASTTSETIQYRKAVKATLVLLPLLIGITMYLMPF	360		
Db 272	YQGPMLVLVLINFIPLFNIRVILMTKLRASTTSETIQYRKAVKATLVLLPLLIGITMYLMPF	331		
Qy 361	VNPGEDSVRVVFIYFNYSFLSPGQGFVSVFYCFINSEVRSAIRKRWHRWQDKHSIRARV	420		
Db 332	VNPGEDSVRVVFIYFNYSFLSPGQGFVSVFYCFINSEVRSAIRKRWHRWQDKHSIRARV	391		
Qy 421	ARAMSIPTSPTRVSFHSIKQSTAV	444		
Db 392	ARAMSIPTSPTRVSFHSIKQSTAV	415		

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RESULT 12
US-09-739-978-4
; Sequence 4, Application US/09739978
; Patent No. 6570140
; GENERAL INFORMATION:
; APPLICANT: The Procter & Gamble Company
; APPLICANT: Isfort, Robert
; APPLICANT: Sheldon, Russell
; APPLICANT:

```



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; TITLE OF INVENTION: Methods for Identifying Compounds for Regulating Muscle Mass and
; FILE REFERENCE: 8448
; CURRENT APPLICATION NUMBER: US/09/799,978
; CURRENT FILING DATE: 2001-03-06
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 415
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-799-978-4

Query Match          91.8%; Score 2186.5; DB 2; Length 415;
Best Local Similarity 93.5%; Pred. No. 5.7e-213;
Matches 415; Conservative 0; Mismatches 0; Indels 29; Gaps 1;

QY 1 MGGHPQLRLVKALLLGLNPVSASLQDQHCESLSLASNISGLQCNASVDLIGTCWPRSPA 60
DB 1 MGGHPQLRLVKALLLGLNPVSASLQDQHCESLSLASNISGLQCNASVDLIGTCWPRSPA 60
QY 61 GOLVVRPCPAFFYGVRYNTTNGYRECLANGSWAARVNYSECQEIINEEKSKVHYHVAV 120
DB 61 GOLVVRPCPAFFYGVRYNTTNGYRECLANGSWAARVNYSECQEIINEEKSKVHYHVAV 120
QY 121 IINYLGHCHISLVALLVAFVFLRLRPGCTHWGDAQDALEVGAPWPGAPFQVRRSIRCLR 180
DB 121 IINYLGHCHISLVALLVAFVFLRLR-----RSIRCLR 151
QY 181 NIHNWNLISAFILRNATFVVLQTMSPVHQSNGVWCRLVTAAYNYFHVNTNPFWMFGEBC 240
DB 152 NIHNWNLISAFILRNATFVVLQTMSPVHQSNGVWCRLVTAAYNYFHVNTNPFWMFGEBC 211
QY 241 YLHTAIVLTYSTDRLRKWMFICIGWGVPPPIIIVAWAIGKLYYDNEKWCWFKRPGVYTDYI 300
DB 212 YLHTAIVLTYSTDRLRKWMFICIGWGVPPPIIIVAWAIGKLYYDNEKWCWFKRPGVYTDYI 271
QY 301 YQGPMLVLLINFIPLFNIRIIMTKLRATSTSETTQYRKAVKATVLLPLLGITTYMLFF 360
DB 272 YQGPMLVLLINFIPLFNIRIIMTKLRATSTSETTQYRKAVKATVLLPLLGITTYMLFF 331
QY 361 VNPGEDEVSRVVIYNSFLESFQGFVSVFYCFLNSEVRSAIRKRWHRWQDKHSIRARV 420
DB 332 VNPGEDEVSRVVIYNSFLESFQGFVSVFYCFLNSEVRSAIRKRWHRWQDKHSIRARV 391
QY 421 ARAMSIPTSPTRVSHSIKQSTAV 444
DB 392 ARAMSIPTSPTRVSHSIKQSTAV 415

RESULT 13
US-09-826-509-483
; Sequence 483, Application US/09826509
; Patent No. 6806054
; GENERAL INFORMATION:
; APPLICANT: Lehmann-Bruinsma, Karin
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lin, I-Lin
; TITLE OF INVENTION: No. 6806054-Endogenous, Constitutively Activated Known G
; FILE REFERENCE: AREN-207
; CURRENT APPLICATION NUMBER: US/09/826,509
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/195,747
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 589
; SOFTWARE: PatentIn Version 2.1
; SEQ ID NO 483
; LENGTH: 415
; TYPE: PRT
; ORGANISM: Homo sapiens
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US-09-826-509-483

Query Match          91.6%; Score 2180.5; DB 2; Length 415;
Best Local Similarity 93.2%; Pred. No. 2.3e-212;
Matches 414; Conservative 0; Mismatches 1; Indels 29; Gaps 1;

QY 1 MGGHPQLRLVKALLLGLNPVSASLQDQHCESLSLASNISGLQCNASVDLIGTCWPRSPA 60
DB 1 MGGHPQLRLVKALLLGLNPVSASLQDQHCESLSLASNISGLQCNASVDLIGTCWPRSPA 60
QY 61 GOLVVRPCPAFFYGVRYNTTNGYRECLANGSWAARVNYSECQEIINEEKSKVHYHVAV 120
DB 61 GOLVVRPCPAFFYGVRYNTTNGYRECLANGSWAARVNYSECQEIINEEKSKVHYHVAV 120
QY 121 IINYLGHCHISLVALLVAFVFLRLRPGCTHWGDAQDALEVGAPWPGAPFQVRRSIRCLR 180
DB 121 IINYLGHCHISLVALLVAFVFLRLR-----RSIRCLR 151
QY 181 NIHNWNLISAFILRNATFVVLQTMSPVHQSNGVWCRLVTAAYNYFHVNTNPFWMFGEBC 240
DB 152 NIHNWNLISAFILRNATFVVLQTMSPVHQSNGVWCRLVTAAYNYFHVNTNPFWMFGEBC 211
QY 241 YLHTAIVLTYSTDRLRKWMFICIGWGVPPPIIIVAWAIGKLYYDNEKWCWFKRPGVYTDYI 300
DB 212 YLHTAIVLTYSTDRLRKWMFICIGWGVPPPIIIVAWAIGKLYYDNEKWCWFKRPGVYTDYI 271
QY 301 YQGPMLVLLINFIPLFNIRIIMTKLRATSTSETTQYRKAVKATVLLPLLGITTYMLFF 360
DB 272 YQGPMLVLLINFIPLFNIRIIMTKLRATSTSETTQYRKAVKATVLLPLLGITTYMLFF 331
QY 361 VNPGEDEVSRVVIYNSFLESFQGFVSVFYCFLNSEVRSAIRKRWHRWQDKHSIRARV 420
DB 332 VNPGEDEVSRVVIYNSFLESFQGFVSVFYCFLNSEVRSAIRKRWHRWQDKHSIRARV 391
QY 421 ARAMSIPTSPTRVSHSIKQSTAV 444
DB 392 ARAMSIPTSPTRVSHSIKQSTAV 415

RESULT 14
US-08-482-746-13
; Sequence 13, Application US/08482746B
; Patent No. 6399315
; GENERAL INFORMATION:
; APPLICANT: Perrin, Marilyn H.
; APPLICANT: Chen, Ruoping
; APPLICANT: Lewis, Kathy A.
; APPLICANT: Vale Jr., Wylie W.
; APPLICANT: Donaldson, Cynthia J.
; APPLICANT: Sawchenko, Paul
; TITLE OF INVENTION: Cloning and Recombinant Production of
; FILE REFERENCE: P41-90002
; CURRENT APPLICATION NUMBER: US/08/482,746B
; EARLIER FILING DATE: 1995-06-07
; EARLIER APPLICATION NUMBER: US 08/374,009
; EARLIER FILING DATE: 1995-01-17
; EARLIER APPLICATION NUMBER: US 08/353,537
; EARLIER FILING DATE: 1994-12-09
; EARLIER APPLICATION NUMBER: PCT/US94/05908
; EARLIER FILING DATE: 1994-05-25
; EARLIER APPLICATION NUMBER: US 08/110,286
; EARLIER FILING DATE: 1993-08-23
; EARLIER APPLICATION NUMBER: US 08/079,320
; EARLIER FILING DATE: 1993-06-18
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 13
; LENGTH: 415
; TYPE: PRT
; ORGANISM: Mus musculus
US-08-482-746-13
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GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: March 16, 2006, 17:21:14 ; Search time 168 Seconds  
(without alignments)  
1104.263 Million cell updates/sec

Title: US-10-649-193-15  
Perfect score: 2381  
Sequence: 1 MGHQPQLRLVKALLLGLNP.....SIPTSPTRVFSHIKSTAV 444

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA\_Main:\*

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2: /cgn2\_6/ptodata/1/pubppaa/US08\_PUBCOMB.pap:\*

3: /cgn2\_6/ptodata/1/pubppaa/US09\_PUBCOMB.pap:\*

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6: /cgn2\_6/ptodata/1/pubppaa/US11\_PUBCOMB.pap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2381	100.0	444	3	US-09-853-386-132
2	2381	100.0	444	3	US-09-853-386-136
3	2381	100.0	444	3	US-09-191-724-15
4	2381	100.0	444	4	US-10-242-822B-2
5	2381	100.0	444	4	US-10-649-193-15
6	2324	97.6	447	4	US-10-232-798-708
7	2186.5	91.8	415	3	US-09-191-724-2
8	2186.5	91.8	415	3	US-09-799-978-2
9	2186.5	91.8	415	3	US-09-799-978-4
10	2186.5	91.8	415	4	US-10-242-822B-1
11	2186.5	91.8	415	4	US-10-649-193-2
12	2186.5	91.8	415	4	US-10-649-852-2
13	2186.5	91.8	415	4	US-10-649-852-4
14	2186.5	91.8	415	4	US-10-450-977-14
15	2180.5	91.6	415	3	US-09-826-509-483
16	2180.5	91.6	415	5	US-10-925-095-483
17	2137.5	89.8	415	3	US-09-853-386-131
18	2137.5	89.8	415	3	US-09-853-386-137
19	2137.5	89.8	415	3	US-09-853-386-138
20	2137.5	89.8	415	3	US-09-191-724-13
21	2137.5	89.8	415	3	US-09-799-978-22
22	2137.5	89.8	415	4	US-10-242-822B-9
23	2137.5	89.8	415	4	US-10-649-193-13
24	2137.5	89.8	415	4	US-10-649-852-22
25	2126.5	89.3	415	3	US-09-853-386-130
26	2126.5	89.3	415	3	US-09-853-386-133
27	2126.5	89.3	415	3	US-09-853-386-134

28	2126.5	89.3	415	3	US-09-191-724-6
29	2126.5	89.3	415	3	US-09-818-009-10
30	2126.5	89.3	415	3	US-09-799-978-16
31	2126.5	89.3	415	3	US-09-799-978-40
32	2126.5	89.3	415	4	US-10-649-193-6
33	2126.5	89.3	415	4	US-10-649-852-16
34	2126.5	89.3	415	4	US-10-649-852-40
35	2092.5	87.9	401	3	US-09-853-386-127
36	2092.5	87.9	401	3	US-09-853-386-139
37	2092.5	87.9	401	3	US-09-799-978-8
38	2092.5	87.9	401	4	US-10-242-822B-4
39	2092.5	87.9	401	4	US-10-649-852-8
40	2086.5	87.6	415	3	US-09-853-386-128
41	2086.5	87.6	415	3	US-09-799-978-28
42	2086.5	87.6	415	4	US-10-649-852-28
43	1945	81.7	420	3	US-09-853-386-129
44	1945	81.7	420	3	US-09-799-978-42
45	1945	81.7	420	4	US-10-649-852-42

ALIGNMENTS

RESULT 1  
US-09-853-386-132  
; Sequence 132, Application US/09853386  
; Patent No. US20020049151A1  
; GENERAL INFORMATION:  
; APPLICANT: Murphy, Evelyn  
; APPLICANT: Breenihan, Barry  
; APPLICANT: Conneely, Orla  
; APPLICANT: Fitzgerald, Oliver  
; TITLE OF INVENTION: Therapeutic Approaches to Diseases by Suppression of the NURR  
; FILE REFERENCES: P01972US1  
; CURRENT APPLICATION NUMBER: US/09/853,386  
; CURRENT FILING DATE: 2001-05-11  
; PRIOR APPLICATION NUMBER: US 60/203645  
; PRIOR FILING DATE: 2000-05-12  
; NUMBER OF SEQ ID NOS: 153  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 132  
; LENGTH: 444  
; TYPE: PRT  
; ORGANISM: HUMAN  
; US-09-853-386-132

Query Match	100.0%;	Score 2381;	DB 3;	Length 444;
Best Local Similarity	100.0%;	Pred. No. 1.7e-217;	Mismatches 0;	Indels 0; Gaps 0;
Matches 444;	Conservative 0;			
QY	1	MGHPQLRLVKALLLGLNPVSASLQDQHCEISLASNISGLQCNASVDLIGTCWPRSPA	60	
Db	1	MGHPQLRLVKALLLGLNPVSASLQDQHCEISLASNISGLQCNASVDLIGTCWPRSPA	60	
QY	61	GLVVRPCPAFFVGYRYNTNNYRECLANGSWAARVNYSECQILNEEKSKVHYHVV	120	
Db	61	GLVVRPCPAFFVGYRYNTNNYRECLANGSWAARVNYSECQILNEEKSKVHYHVV	120	
QY	121	IINYLGHCISLVALLVAFVFLRLRPGCTHWGDOAGALEVGAPWSGAPFQVRKSIICLR	180	
Db	121	IINYLGHCISLVALLVAFVFLRLRPGCTHWGDOAGALEVGAPWSGAPFQVRKSIICLR	180	
QY	181	NIHWNLSIFILRNATFVQVLTMSPEVHQSNVGCRLVTAAYNYFHTNFFWMFGEBC	240	
Db	181	NIHWNLSIFILRNATFVQVLTMSPEVHQSNVGCRLVTAAYNYFHTNFFWMFGEBC	240	
QY	241	YLHTAIVLTSTDRLRKMFICIGWVPPFIIVAWAIGKLYYDNEKCFWPKRGVYTDYI	300	
Db	241	YLHTAIVLTSTDRLRKMFICIGWVPPFIIVAWAIGKLYYDNEKCFWPKRGVYTDYI	300	
QY	301	YQCPMLIVLLINFTFLFNIVRLMTKLRASTTETIQYRKAVKATLVLLPLLGITYMLFF	360	

Db 301 YQGPMLVLLNIFLFIPLNIVIRILMTKLRASSTTQYRKAVKATVLLPLLGITYMLPF 360  
Qy 361 VNPGEVSRVVIYFNPSFLESQGFVSVFYCFNLSEVRSAIRKRWHRWQDKHSIRARV 420  
Db 361 VNPGEVSRVVIYFNPSFLESQGFVSVFYCFNLSEVRSAIRKRWHRWQDKHSIRARV 420  
Qy 421 ARAMSIPTSPTRVSVFHSIKQSTAV 444  
Db 421 ARAMSIPTSPTRVSVFHSIKQSTAV 444

RESULT 2  
US-09-853-386-136  
; Sequence 136, Application US/09853386  
; Patent No. US20020049151A1  
; GENERAL INFORMATION:  
; APPLICANT: Murphy, Evelyn  
; APPLICANT: Bresnahan, Barry  
; APPLICANT: Conneely, Orla  
; APPLICANT: Fitzgerald, Oliver  
; TITLE OF INVENTION: Therapeutic Approaches to Diseases by Suppression of the NURR  
; FILE REFERENCE: P01972U51  
; CURRENT APPLICATION NUMBER: US/09/853,386  
; PRIOR FILING DATE: 2001-05-11  
; PRIOR APPLICATION NUMBER: US 60/203645  
; PRIOR FILING DATE: 2000-05-12  
; NUMBER OF SEQ ID NOS: 153  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 136  
; LENGTH: 444  
; TYPE: PRT  
; ORGANISM: HUMAN  
US-09-853-386-136

Query Match 100.0%; Score 2381; DB 3; Length 444;  
Best Local Similarity 100.0%; Pred. No. 1.7e-217;  
Matches 444; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGGHPQLRLVKALLLGLNPNVSLQDQHCESLSLASNISGLQCNASVDLIGTCWPRSPA 60  
Db 1 MGGHPQLRLVKALLLGLNPNVSLQDQHCESLSLASNISGLQCNASVDLIGTCWPRSPA 60  
Qy 61 GQLVVRPCPAFFYGVRYNTTNGYRECLANGSNAARVNYSECEIILNEEKSKVHYHVAV 120  
Db 61 GQLVVRPCPAFFYGVRYNTTNGYRECLANGSNAARVNYSECEIILNEEKSKVHYHVAV 120  
Qy 121 IINYLGHICISLVALLVAFVFLRLRPGCTHWGDAQDGALEVGAPWGSAPQVRRSIRCLR 180  
Db 121 IINYLGHICISLVALLVAFVFLRLRPGCTHWGDAQDGALEVGAPWGSAPQVRRSIRCLR 180  
Qy 181 NIHNWNLISAFILRNATWVQVLTMSPEVHQSNVGCRLVTAAYNYFHVTFNFMFGEBC 240  
Db 181 NIHNWNLISAFILRNATWVQVLTMSPEVHQSNVGCRLVTAAYNYFHVTFNFMFGEBC 240  
Qy 241 YLHTAIVLTYSTDRLRKWMFICIGWGPPIIVAMAIGKLYDNEKCFWKGKRPVYTDYI 300  
Db 241 YLHTAIVLTYSTDRLRKWMFICIGWGPPIIVAMAIGKLYDNEKCFWKGKRPVYTDYI 300  
Qy 301 YQGPMLVLLNIFLFIPLNIVIRILMTKLRASSTTQYRKAVKATVLLPLLGITYMLPF 360  
Db 301 YQGPMLVLLNIFLFIPLNIVIRILMTKLRASSTTQYRKAVKATVLLPLLGITYMLPF 360  
Qy 361 VNPGEVSRVVIYFNPSFLESQGFVSVFYCFNLSEVRSAIRKRWHRWQDKHSIRARV 420  
Db 361 VNPGEVSRVVIYFNPSFLESQGFVSVFYCFNLSEVRSAIRKRWHRWQDKHSIRARV 420  
Qy 421 ARAMSIPTSPTRVSVFHSIKQSTAV 444  
Db 421 ARAMSIPTSPTRVSVFHSIKQSTAV 444

RESULT 3

US-09-191-724-15  
; Sequence 15, Application US/09191724  
; Patent No. US20020055617A1  
; GENERAL INFORMATION:  
; APPLICANT: Perrin, Marilyn H.  
; APPLICANT: Chen, Ruoping  
; APPLICANT: Lewis, Kathy A.  
; APPLICANT: Vale Jr., Wylie W.  
; APPLICANT: Donaldson, Cynthia J.  
; APPLICANT: Sawchenko, Paul  
; TITLE OF INVENTION: Cloning and Recombinant Production of  
; FILE REFERENCE: CRF Receptor(s)  
; CURRENT APPLICATION NUMBER: US/09/191,724  
; CURRENT FILING DATE: 1998-11-12  
; EARLIER APPLICATION NUMBER: US 08/374,009  
; EARLIER FILING DATE: 1995-01-17  
; EARLIER APPLICATION NUMBER: US 08/353,537  
; EARLIER FILING DATE: 1994-12-09  
; EARLIER APPLICATION NUMBER: PCT/US94/05908  
; EARLIER FILING DATE: 1993-05-25  
; EARLIER APPLICATION NUMBER: US 08/110,286  
; EARLIER FILING DATE: 1993-08-23  
; EARLIER APPLICATION NUMBER: US 08/079,320  
; EARLIER FILING DATE: 1993-06-18  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: PastSeq for Windows Version 3.0  
; SEQ ID NO 15  
; LENGTH: 444  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-191-724-15

Query Match 100.0%; Score 2381; DB 3; Length 444;  
Best Local Similarity 100.0%; Pred. No. 1.7e-217;  
Matches 444; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGGHPQLRLVKALLLGLNPNVSLQDQHCESLSLASNISGLQCNASVDLIGTCWPRSPA 60  
Db 1 MGGHPQLRLVKALLLGLNPNVSLQDQHCESLSLASNISGLQCNASVDLIGTCWPRSPA 60  
Qy 61 GQLVVRPCPAFFYGVRYNTTNGYRECLANGSNAARVNYSECEIILNEEKSKVHYHVAV 120  
Db 61 GQLVVRPCPAFFYGVRYNTTNGYRECLANGSNAARVNYSECEIILNEEKSKVHYHVAV 120  
Qy 121 IINYLGHICISLVALLVAFVFLRLRPGCTHWGDAQDGALEVGAPWGSAPQVRRSIRCLR 180  
Db 121 IINYLGHICISLVALLVAFVFLRLRPGCTHWGDAQDGALEVGAPWGSAPQVRRSIRCLR 180  
Qy 181 NIHNWNLISAFILRNATWVQVLTMSPEVHQSNVGCRLVTAAYNYFHVTFNFMFGEBC 240  
Db 181 NIHNWNLISAFILRNATWVQVLTMSPEVHQSNVGCRLVTAAYNYFHVTFNFMFGEBC 240  
Qy 241 YLHTAIVLTYSTDRLRKWMFICIGWGPPIIVAMAIGKLYDNEKCFWKGKRPVYTDYI 300  
Db 241 YLHTAIVLTYSTDRLRKWMFICIGWGPPIIVAMAIGKLYDNEKCFWKGKRPVYTDYI 300  
Qy 301 YQGPMLVLLNIFLFIPLNIVIRILMTKLRASSTTQYRKAVKATVLLPLLGITYMLPF 360  
Db 301 YQGPMLVLLNIFLFIPLNIVIRILMTKLRASSTTQYRKAVKATVLLPLLGITYMLPF 360  
Qy 361 VNPGEVSRVVIYFNPSFLESQGFVSVFYCFNLSEVRSAIRKRWHRWQDKHSIRARV 420  
Db 361 VNPGEVSRVVIYFNPSFLESQGFVSVFYCFNLSEVRSAIRKRWHRWQDKHSIRARV 420  
Qy 421 ARAMSIPTSPTRVSVFHSIKQSTAV 444  
Db 421 ARAMSIPTSPTRVSVFHSIKQSTAV 444

RESULT 4  
US-10-242-8228-2  
; Sequence 2, Application US/10242822B

Publication No. US20030113799A1  
; GENERAL INFORMATION:  
; APPLICANT: Pisarchik, Alexander  
; APPLICANT: Slominski, Andrzej  
; TITLE OF INVENTION: Variants of Corticotropin Releasing Hormone  
; TITLE OF INVENTION: Receptor Type 1 and Uses Thereof  
; FILE REFERENCE: D6420  
; CURRENT APPLICATION NUMBER: US/10/242,822B  
; CURRENT FILING DATE: 2002-12-09  
; PRIOR APPLICATION NUMBER: US 60/322,195  
; PRIOR FILING DATE: 2001-09-14  
; NUMBER OF SEQ ID NOS: 49  
; SEQ ID NO 2  
; LENGTH: 444  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: amino acid sequence of human CRH-R1 beta  
; OTHER INFORMATION: gene: GenBank Accession No. US20030113799A1 L23333  
US-10-242-822B-2

Query Match 100.0%; Score 2381; DB 4; Length 444;  
Best Local Similarity 100.0%; Pred. No. 1.7e-217;  
Matches 444; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MGHPQLRLVKALLLGLNPVSASLQDHCHESLSLASNISGLQCNASVDLIGTCWPRSPA	60
DB	1	MGHPQLRLVKALLLGLNPVSASLQDHCHESLSLASNISGLQCNASVDLIGTCWPRSPA	60
QY	61	GLAVRCPAPFFGVRYNTTNGYRECLANGSWAARVNYSECOILNEEKSKVHYHAV	120
DB	61	GLAVRCPAPFFGVRYNTTNGYRECLANGSWAARVNYSECOILNEEKSKVHYHAV	120
QY	121	IINYLGHCHISLVALLVAFVFLRLRPGCTHWGDAQDGALEVGAPWPGAPQVRRSIRCLR	180
DB	121	IINYLGHCHISLVALLVAFVFLRLRPGCTHWGDAQDGALEVGAPWPGAPQVRRSIRCLR	180
QY	181	NIHWNLSAFILRNATWFFVQLTMSPEVHQSNGVWCRLVTAAYNYPHVTNPFMMFGECC	240
DB	181	NIHWNLSAFILRNATWFFVQLTMSPEVHQSNGVWCRLVTAAYNYPHVTNPFMMFGECC	240
QY	241	YLTAIVLTYSTDLRKNMFCICGWGVPPIIIVAWAIGKLYDNEKCFGRPGVYTDYI	300
DB	241	YLTAIVLTYSTDLRKNMFCICGWGVPPIIIVAWAIGKLYDNEKCFGRPGVYTDYI	300
QY	301	YQGPMLVLLINFIPLFNIVRLMTKLRASTTSETIQYKAVKATLVLLPLLGITYMLFF	360
DB	301	YQGPMLVLLINFIPLFNIVRLMTKLRASTTSETIQYKAVKATLVLLPLLGITYMLFF	360
QY	361	VNPGDEVSRRVFIYFNSFLESFGQFPFVSFYCYFLNSEVRSAIRKRWHRWDKHSIRARV	420
DB	361	VNPGDEVSRRVFIYFNSFLESFGQFPFVSFYCYFLNSEVRSAIRKRWHRWDKHSIRARV	420
QY	421	ARAMSIPTSPTRVSPHSIKQSTAV 444	
DB	421	ARAMSIPTSPTRVSPHSIKQSTAV 444	

RESULT 6  
US-10-292-798-708  
; Sequence 708, Application US/10292798  
; Publication No. US20030235833A1  
; GENERAL INFORMATION:  
; APPLICANT: SUWA, MAKIKO  
; APPLICANT: ASAI, KIYOSHI  
; APPLICANT: AKIYAMA, YUTAKA  
; APPLICANT: ABEURATANI, HIROYUKI  
; TITLE OF INVENTION: GUANOSINE TRIPHOSPHATE-BINDING PROTEIN COUPLED RECEPTORS  
; FILE REFERENCE: 084335/166  
; CURRENT APPLICATION NUMBER: US/10/292,798  
; CURRENT FILING DATE: 2002-11-13  
; PRIOR APPLICATION NUMBER: 10/017,161  
; PRIOR FILING DATE: 2001-12-18

RESULT 5  
US-10-649-193-15  
; Sequence 15, Application US/10649193  
; Publication No. US20040039173A1  
; GENERAL INFORMATION:  
; APPLICANT: Perrin, Marilyn H.  
; APPLICANT: Chen, Ruoping  
; APPLICANT: Lewis, Kathy A.  
; APPLICANT: Vale Jr., Wylie W.  
; APPLICANT: Donaldson, Cynthia J.  
; APPLICANT: Sawchenko, Paul  
; TITLE OF INVENTION: Cloning and Recombinant Production of  
; TITLE OF INVENTION: CRF Receptor(s)  
; FILE REFERENCE: Salk1748  
; CURRENT APPLICATION NUMBER: US/10/649,193

;  
; PRIOR APPLICATION NUMBER: JP 2001-246789  
; PRIOR FILING DATE: 2001-06-18  
; NUMBER OF SEQ ID NOS: 2070  
; SOFTWARE: Patent in Ver. 2.1  
; SEQ ID NO 708  
; LENGTH: 447  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-292-798-708

Query Match 97.6%; Score 2324; DB 4; Length 447;  
Best Local Similarity 99.8%; Pred. No. 4.6e-212;  
Matches 433; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
QY 11 KALLLLGLNPVSASLQDQHCHESLSLASNISGLQCNASVDLIGTCWPRSPAGLVVRPCPA 70  
DB 14 RALLLLGLNPVSASLQDQHCHESLSLASNISGLQCNASVDLIGTCWPRSPAGLVVRPCPA 73  
  
QY 71 FFYGVRYNTTNGYRECLANGSWAARVNYSECQEIILNEEKSKVHYHVAVIINYLGHCHIS 130  
DB 74 FFYGVRYNTTNGYRECLANGSWAARVNYSECQEIILNEEKSKVHYHVAVIINYLGHCHIS 133  
  
QY 131 LVALLVAFVFLRLRPGCTHGWDAQDGALEVGAPWPGAPQVRRSIRCLNIIHMNLISA 190  
DB 134 LVALLVAFVFLRLRPGCTHGWDAQDGALEVGAPWPGAPQVRRSIRCLNIIHMNLISA 193  
  
QY 191 FILRNATFWVQLTMSPEVHQSNGVCRVLTAAVNYFHVNTNPFWMFGECCYLHTAIVLTY 250  
DB 194 FILRNATFWVQLTMSPEVHQSNGVCRVLTAAVNYFHVNTNPFWMFGECCYLHTAIVLTY 253  
  
QY 251 STDRLRKWPFICIGWGVPPPIIVAMAIGKLYYDNEKCMFGKRGVYTDYIYQGPMLVLL 310  
DB 254 STDRLRKWPFICIGWGVPPPIIVAMAIGKLYYDNEKCMFGKRGVYTDYIYQGPMLVLL 313  
  
QY 311 INFIFLNVIRILMTKLRASTTSETTOYRKAVKATVLLPLLGITTYMLFPVNPGEDEVSR 370  
DB 314 INFIFLNVIRILMTKLRASTTSETTOYRKAVKATVLLPLLGITTYMLFPVNPGEDEVSR 373  
  
QY 371 VFIYNSFLESFQGFVSVFYFCFLNSEVRSARKEWHRWQDKHSIRARVARMSIPTSP 430  
DB 374 VFIYNSFLESFQGFVSVFYFCFLNSEVRSARKEWHRWQDKHSIRARVARMSIPTSP 433  
  
QY 431 TRVSPHSIKQSTAV 444  
DB 434 TRVSPHSIKQSTAV 447

RESULT 7  
US-09-191-724-2  
; Sequence 2, Application US/09191724  
; Patent No. US20020055617A1  
; GENERAL INFORMATION:  
; APPLICANT: Perrin, Marilyn H.  
; APPLICANT: Chen, Ruoping  
; APPLICANT: Lewis, Kathy A.  
; APPLICANT: Vale Jr., Wylie W.  
; APPLICANT: Donaldson, Cynthia J.  
; APPLICANT: Sawchenko, Paul  
; TITLE OF INVENTION: Cloning and Recombinant Production of  
; FILE OF INVENTION: CRF Receptor(s)  
; FILE REFERENCE: Salk1748  
; CURRENT APPLICATION NUMBER: US/09/191,724  
; EARLIER APPLICATION NUMBER: 1998-11-12  
; EARLIER FILING DATE: 1998-11-12  
; EARLIER APPLICATION NUMBER: US 08/374,009  
; EARLIER FILING DATE: 1995-01-17  
; EARLIER APPLICATION NUMBER: US 08/353,537  
; EARLIER FILING DATE: 1994-12-09  
; EARLIER APPLICATION NUMBER: PCT/US94/05908  
; EARLIER FILING DATE: 1993-05-25  
; EARLIER APPLICATION NUMBER: US 08/110,286  
; EARLIER FILING DATE: 1993-08-23  
; EARLIER APPLICATION NUMBER: US 08/079,320  
; EARLIER FILING DATE: 1993-06-18

;  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 2  
; LENGTH: 415  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-191-724-2

Query Match 91.8%; Score 2186.5; DB 3; Length 415;  
Best Local Similarity 93.5%; Pred. No. 5e-199;  
Matches 415; Conservative 0; Mismatches 0; Indels 29; Gaps 1;  
  
QY 1 MGGHPQLRLVKALLLGLNPVSASLQDQHCHESLSLASNISGLQCNASVDLIGTCWPRSPA 60  
DB 1 MGGHPQLRLVKALLLGLNPVSASLQDQHCHESLSLASNISGLQCNASVDLIGTCWPRSPA 60  
  
QY 61 GQLVVRPCPAFFYGVRYNTTNGYRECLANGSWAARVNYSECQEIILNEEKSKVHYHVAV 120  
DB 61 GQLVVRPCPAFFYGVRYNTTNGYRECLANGSWAARVNYSECQEIILNEEKSKVHYHVAV 120  
  
QY 121 IINYLGHCHISLVALLVAFVFLRLRPGCTHGWDAQDGALEVGAPWPGAPQVRRSIRCLR 180  
DB 121 IINYLGHCHISLVALLVAFVFLRLRPGCTHGWDAQDGALEVGAPWPGAPQVRRSIRCLR 180  
  
QY 181 NIIHMNLISAFILRNATFWVQLTMSPEVHQSNGVCRVLTAAVNYFHVNTNPFWMFGECC 240  
DB 152 NIIHMNLISAFILRNATFWVQLTMSPEVHQSNGVCRVLTAAVNYFHVNTNPFWMFGECC 211  
  
QY 241 YLHTAIVLTYSTDRLRKWPFICIGWGVPPPIIVAMAIGKLYYDNEKCMFGKRGVYTDYI 300  
DB 212 YLHTAIVLTYSTDRLRKWPFICIGWGVPPPIIVAMAIGKLYYDNEKCMFGKRGVYTDYI 271  
  
QY 301 YQGPMLVLLINFIFLNVIRILMTKLRASTTSETTOYRKAVKATVLLPLLGITTYMLFF 360  
DB 272 YQGPMLVLLINFIFLNVIRILMTKLRASTTSETTOYRKAVKATVLLPLLGITTYMLFF 331  
  
QY 361 VNPGEDEVSRVFIYNSFLESFQGFVSVFYFCFLNSEVRSARKEWHRWQDKHSIRARV 420  
DB 332 VNPGEDEVSRVFIYNSFLESFQGFVSVFYFCFLNSEVRSARKEWHRWQDKHSIRARV 391  
  
QY 421 ARAMSIPTSPTRVSPHSIKQSTAV 444  
DB 392 ARAMSIPTSPTRVSPHSIKQSTAV 415

RESULT 8  
US-09-799-978-2  
; Sequence 2, Application US/09799978  
; Publication No. US20030165807A1  
; GENERAL INFORMATION:  
; APPLICANT: The Procter & Gamble Company  
; APPLICANT: Isfort, Robert  
; APPLICANT: Sheldon, Russell  
; TITLE OF INVENTION: Methods for Identifying Compounds for Regulating Muscle Mass or  
; TITLE OF INVENTION: Function Using Corticotropin Releasing Factor Receptors  
; FILE REFERENCE: 8448  
; CURRENT APPLICATION NUMBER: US/09/799,978  
; CURRENT FILING DATE: 2001-03-06  
; NUMBER OF SEQ ID NOS: 44  
; SOFTWARE: Patent In version 3.0  
; SEQ ID NO 2  
; LENGTH: 415  
; TYPE: PRT  
; ORGANISM: homo sapiens  
US-09-799-978-2  
  
Query Match 91.8%; Score 2186.5; DB 3; Length 415;  
Best Local Similarity 93.5%; Pred. No. 5e-199;  
Matches 415; Conservative 0; Mismatches 0; Indels 29; Gaps 1;  
  
QY 1 MGGHPQLRLVKALLLGLNPVSASLQDQHCHESLSLASNISGLQCNASVDLIGTCWPRSPA 60  
DB 1 MGGHPQLRLVKALLLGLNPVSASLQDQHCHESLSLASNISGLQCNASVDLIGTCWPRSPA 60

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QY 61 GQLVVRPCPAFFYGVRYNTTNGYRECLANGSWAARVNYSECQIILNEEKSKVHHVAV 120
|
|
|
Db 61 GQLVVRPCPAFFYGVRYNTTNGYRECLANGSWAARVNYSECQIILNEEKSKVHHVAV 120
|
|
|
QY 121 IINYLGHGISLVALLVAFVLFRLRPGCTHWGDAQDGALEVGAPWSGAPQVRRSIRCLR 180
|
|
|
Db 121 IINYLGHGISLVALLVAFVLFRLR-----RSIRCLR 151
|
|
|
QY 181 NIHWNLISAFILRNATFVQVLTMSPEVHQSNVGCRLVTAAYNYFHVNTFFWMFGECC 240
|
|
|
Db 152 NIHWNLISAFILRNATFVQVLTMSPEVHQSNVGCRLVTAAYNYFHVNTFFWMFGECC 211
|
|
|
QY 241 YLHTAIVLTSTDRLRKMPICIGWGPVPIIIVAWAIGKLYYDNEKCFGRPGVYTDYI 300
|
|
|
Db 212 YLHTAIVLTSTDRLRKMPICIGWGPVPIIIVAWAIGKLYYDNEKCFGRPGVYTDYI 271
|
|
|
QY 301 YQGPMLVLLINFIPLFNIVRIILMTKLRASTTSETIQRKAVKATLVLLPLLGITMYLFF 360
|
|
|
Db 272 YQGPMLVLLINFIPLFNIVRIILMTKLRASTTSETIQRKAVKATLVLLPLLGITMYLFF 331
|
|
|
QY 361 VNPGEDEVSRVVIYFNSFLESQGFVSVFYCFNLSEVRSAIRKRWHRQDKHSIRARV 420
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Db 332 VNPGEDEVSRVVIYFNSFLESQGFVSVFYCFNLSEVRSAIRKRWHRQDKHSIRARV 391
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|
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QY 421 ARAMSIPTSPTRVSVFHSIKQSTAV 444
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Db 392 ARAMSIPTSPTRVSVFHSIKQSTAV 415
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RESULT 9
US-09-799-978-4
; Sequence 4, Application US/09799978
; Publication No. US20030165807A1
; GENERAL INFORMATION:
; APPLICANT: The Procter & Gamble Company
; APPLICANT: Isfort, Robert
; TITLE OF INVENTION: Methods for Identifying Compounds for Regulating Muscle Mass and
; TITLE OF INVENTION: Function Using Corticotropin Releasing Factor Receptors
; FILE REFERENCE: 8448
; CURRENT APPLICATION NUMBER: US/09/799,978
; CURRENT FILING DATE: 2001-03-06
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 415
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-799-978-4
Query Match 91.8%; Score 2186.5; DB 3; Length 415;
Best Local Similarity 93.5%; Pred. No. 5e-199;
Matches 415; Conservative 0; Mismatches 0; Indels 29; Gaps 1;
QY 1 MGGHPQLRLVKALLLGLNLPVSASLQDQHCESLSLASNISGLQCNASVDLIGTCWPRSPA 60
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Db 1 MGGHPQLRLVKALLLGLNLPVSASLQDQHCESLSLASNISGLQCNASVDLIGTCWPRSPA 60
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Db 61 GQLVVRPCPAFFYGVRYNTTNGYRECLANGSWAARVNYSECQIILNEEKSKVHHVAV 120
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Db 121 IINYLGHGISLVALLVAFVLFRLR-----RSIRCLR 151
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QY 181 NIHWNLISAFILRNATFVQVLTMSPEVHQSNVGCRLVTAAYNYFHVNTFFWMFGECC 240
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Db 152 NIHWNLISAFILRNATFVQVLTMSPEVHQSNVGCRLVTAAYNYFHVNTFFWMFGECC 211
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QY 241 YLHTAIVLTSTDRLRKMPICIGWGPVPIIIVAWAIGKLYYDNEKCFGRPGVYTDYI 300
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Db 272 YQGPMLVLLINFIPLFNIVRIILMTKLRASTTSETIQRKAVKATLVLLPLLGITMYLFF 331
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Db 332 VNPGEDEVSRVVIYFNSFLESQGFVSVFYCFNLSEVRSAIRKRWHRQDKHSIRARV 391
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QY 421 ARAMSIPTSPTRVSVFHSIKQSTAV 444
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Db 392 ARAMSIPTSPTRVSVFHSIKQSTAV 415
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RESULT 9
US-09-799-978-4
; Sequence 4, Application US/09799978
; Publication No. US20030165807A1
; GENERAL INFORMATION:
; APPLICANT: The Procter & Gamble Company
; APPLICANT: Isfort, Robert
; TITLE OF INVENTION: Methods for Identifying Compounds for Regulating Muscle Mass and
; TITLE OF INVENTION: Function Using Corticotropin Releasing Factor Receptors
; FILE REFERENCE: 8448
; CURRENT APPLICATION NUMBER: US/09/799,978
; CURRENT FILING DATE: 2001-03-06
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 415
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-799-978-4
Query Match 91.8%; Score 2186.5; DB 3; Length 415;
Best Local Similarity 93.5%; Pred. No. 5e-199;
Matches 415; Conservative 0; Mismatches 0; Indels 29; Gaps 1;
QY 1 MGGHPQLRLVKALLLGLNLPVSASLQDQHCESLSLASNISGLQCNASVDLIGTCWPRSPA 60
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Db 1 MGGHPQLRLVKALLLGLNLPVSASLQDQHCESLSLASNISGLQCNASVDLIGTCWPRSPA 60
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QY 61 GQLVVRPCPAFFYGVRYNTTNGYRECLANGSWAARVNYSECQIILNEEKSKVHHVAV 120
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Db 61 GQLVVRPCPAFFYGVRYNTTNGYRECLANGSWAARVNYSECQIILNEEKSKVHHVAV 120
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Db 121 IINYLGHGISLVALLVAFVLFRLR-----RSIRCLR 151
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Db 152 NIHWNLISAFILRNATFVQVLTMSPEVHQSNVGCRLVTAAYNYFHVNTFFWMFGECC 211
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QY 241 YLHTAIVLTSTDRLRKMPICIGWGPVPIIIVAWAIGKLYYDNEKCFGRPGVYTDYI 300
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Db 212 YLHTAIVLTSTDRLRKMPICIGWGPVPIIIVAWAIGKLYYDNEKCFGRPGVYTDYI 271
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QY 361 VNPGEDEVSRVVIYFNSFLESQGFVSVFYCFNLSEVRSAIRKRWHRQDKHSIRARV 420
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Db 332 VNPGEDEVSRVVIYFNSFLESQGFVSVFYCFNLSEVRSAIRKRWHRQDKHSIRARV 391
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QY 421 ARAMSIPTSPTRVSVFHSIKQSTAV 444
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Db 392 ARAMSIPTSPTRVSVFHSIKQSTAV 415
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RESULT 10
US-10-242-822B-1
; Sequence 1, Application US/10242822B
; Publication No. US20030113799A1
; GENERAL INFORMATION:
; APPLICANT: Pleschik, Alexander
; APPLICANT: Slominski, Andrzej
; TITLE OF INVENTION: Variants of Corticotropin Releasing Hormone
; TITLE OF INVENTION: Receptor Type 1 and Uses Thereof
; FILE REFERENCE: D6420
; CURRENT APPLICATION NUMBER: US/10/242,822B
; CURRENT FILING DATE: 2002-12-09
; PRIOR APPLICATION NUMBER: US 60/322,195
; PRIOR FILING DATE: 2001-09-14
; NUMBER OF SEQ ID NOS: 49
; SEQ ID NO 1
; LENGTH: 415
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: amino acid sequence of human CRH-R1 alpha
; OTHER INFORMATION: Gene: GenBank Accession No. US20030113799A1 L23332
US-10-242-822B-1
Query Match 91.8%; Score 2186.5; DB 4; Length 415;
Best Local Similarity 93.5%; Pred. No. 5e-199;
Matches 415; Conservative 0; Mismatches 0; Indels 29; Gaps 1;
QY 1 MGGHPQLRLVKALLLGLNLPVSASLQDQHCESLSLASNISGLQCNASVDLIGTCWPRSPA 60
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Db 1 MGGHPQLRLVKALLLGLNLPVSASLQDQHCESLSLASNISGLQCNASVDLIGTCWPRSPA 60
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QY 61 GQLVVRPCPAFFYGVRYNTTNGYRECLANGSWAARVNYSECQIILNEEKSKVHHVAV 120
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Db 61 GQLVVRPCPAFFYGVRYNTTNGYRECLANGSWAARVNYSECQIILNEEKSKVHHVAV 120
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QY 121 IINYLGHGISLVALLVAFVLFRLRPGCTHWGDAQDGALEVGAPWSGAPQVRRSIRCLR 180
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Db 121 IINYLGHGISLVALLVAFVLFRLR-----RSIRCLR 151
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QY 181 NIHWNLISAFILRNATFVQVLTMSPEVHQSNVGCRLVTAAYNYFHVNTFFWMFGECC 240
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Db 152 NIHWNLISAFILRNATFVQVLTMSPEVHQSNVGCRLVTAAYNYFHVNTFFWMFGECC 211
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QY 241 YLHTAIVLTSTDRLRKMPICIGWGPVPIIIVAWAIGKLYYDNEKCFGRPGVYTDYI 300
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Db 212 YLHTAIVLTSTDRLRKMPICIGWGPVPIIIVAWAIGKLYYDNEKCFGRPGVYTDYI 271
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QY 301 YQGPMLVLLINFIPLFNIVRIILMTKLRASTTSETIQRKAVKATLVLLPLLGITMYLFF 360
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Db 272 YQGPMLVLLINFIPLFNIVRIILMTKLRASTTSETIQRKAVKATLVLLPLLGITMYLFF 331
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QY 361 VNPGEDEVSRVVIYFNSFLESQGFVSVFYCFNLSEVRSAIRKRWHRQDKHSIRARV 420
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Db 332 VNPGEDEVSRVVIYFNSFLESQGFVSVFYCFNLSEVRSAIRKRWHRQDKHSIRARV 391
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QY 421 ARAMSIPTSPTRVSVFHSIKQSTAV 444
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Db 392 ARAMSIPTSPTRVSPHSIKQSTAV 415

## RESULT 11

US-10-649-193-2

; Sequence 2, Application US/10649193

; Publication No. US20040039173A1

; GENERAL INFORMATION:

; APPLICANT: Perrin, Marilyn H.

; APPLICANT: Chen, Ruoping A.

; APPLICANT: Lewis, Kathy A.

; APPLICANT: Vale Jr., Wylie W.

; APPLICANT: Donaldson, Cynthia J.

; APPLICANT: Sawchenko, Paul

; TITLE OF INVENTION: Cloning and Recombinant Production of

; TITLE OF INVENTION: CRF Receptor(s)

; FILE REFERENCE: Salk1748

; CURRENT APPLICATION NUMBER: US/10/649,193

; CURRENT FILING DATE: 2003-08-26

; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/191,724

; PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-12

; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 08/374,009

; PRIOR FILING DATE: EARLIER FILING DATE: 1995-01-17

; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 08/353,537

; PRIOR FILING DATE: EARLIER FILING DATE: 1994-12-09

; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: PCT/US94/05908

; PRIOR FILING DATE: EARLIER FILING DATE: 1993-05-25

; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 08/110,286

; PRIOR FILING DATE: EARLIER FILING DATE: 1993-08-23

; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 08/079,320

; PRIOR FILING DATE: EARLIER FILING DATE: 1993-06-18

; NUMBER OF SEQ ID NOS: 15

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 2

; LENGTH: 415

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-649-193-2

## Query Match

Best Local Similarity 91.8%; Score 2186.5; DB 4; Length 415;

Matches 415; Conservative 0; Mismatches 0; Indels 29; Gaps 1;

QY 1 MGGHPQLRLVKALLLGLNPFVSASLQDQHCESLSLASNISGLQCNASVDLIGTCWPRSPA 60

DB 1 MGGHPQLRLVKALLLGLNPFVSASLQDQHCESLSLASNISGLQCNASVDLIGTCWPRSPA 60

QY 61 GQLVVRPCPAFFYGVRYNTTNGYRECLANGSWAARVNYSECOEILNEEKSKVHYHVAV 120

DB 61 GQLVVRPCPAFFYGVRYNTTNGYRECLANGSWAARVNYSECOEILNEEKSKVHYHVAV 120

QY 121 IINYLGHCSLVALLVAFVLFLRLPGCTHWGDQADGALVGPWPGAPQVRRSTRCLR 180

DB 121 IINYLGHCSLVALLVAFVLFLRLPGCTHWGDQADGALVGPWPGAPQVRRSTRCLR 180

QY 181 NIHNWNLISAFILRNATFVVLQVTSPEVHQSVNGWCRLVTAAYNYFHVTFNPFMFGEGC 240

DB 152 NIHNWNLISAFILRNATFVVLQVTSPEVHQSVNGWCRLVTAAYNYFHVTFNPFMFGEGC 211

QY 241 YLHTAIVLTYSTDLRKWMFICIGWGPVPIIIVAMAIGKLYYDNEKCFKRPVGYTDYI 300

DB 212 YLHTAIVLTYSTDLRKWMFICIGWGPVPIIIVAMAIGKLYYDNEKCFKRPVGYTDYI 271

QY 301 YQGPMLVLLINFIPLFNIVRIIMTKLRASSTSETIYQKAVKATLVLLPLGITVMLPFF 360

DB 272 YQGPMLVLLINFIPLFNIVRIIMTKLRASSTSETIYQKAVKATLVLLPLGITVMLPFF 331

QY 361 VNPGEDEVSRVFIYFNSFLESFQGFVSVFYCFNLSEVRSAIRKRWHRWQDKHSIRARV 420

DB 332 VNPGEDEVSRVFIYFNSFLESFQGFVSVFYCFNLSEVRSAIRKRWHRWQDKHSIRARV 391

QY 421 ARAMSIPTSPTRVSPHSIKQSTAV 444

DB 421 ARAMSIPTSPTRVSPHSIKQSTAV 444

Db 392 ARAMSIPTSPTRVSPHSIKQSTAV 415

## RESULT 12

US-10-649-852-2

; Sequence 2, Application US/10649852

; Publication No. US20040101911A1

; GENERAL INFORMATION:

; APPLICANT: The Procter & Gamble Company

; APPLICANT: Isfort, Robert

; APPLICANT: Sheldon, Russell

; TITLE OF INVENTION: Methods for Identifying Compounds for Regulating Muscle Mass or F

; TITLE OF INVENTION: Using Corticotropin Releasing Factor Receptors

; FILE REFERENCE: 8448R

; CURRENT APPLICATION NUMBER: US/10/649,852

; CURRENT FILING DATE: 2003-08-27

; PRIOR APPLICATION NUMBER: US 09/799,978

; PRIOR FILING DATE: 2001-03-06

; NUMBER OF SEQ ID NOS: 44

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 2

; LENGTH: 415

; TYPE: PRT

; ORGANISM: homo sapiens

US-10-649-852-2

## Query Match

Best Local Similarity 91.8%; Score 2186.5; DB 4; Length 415;

Matches 415; Conservative 0; Mismatches 0; Indels 29; Gaps 1;

QY 1 MGGHPQLRLVKALLLGLNPFVSASLQDQHCESLSLASNISGLQCNASVDLIGTCWPRSPA 60

DB 1 MGGHPQLRLVKALLLGLNPFVSASLQDQHCESLSLASNISGLQCNASVDLIGTCWPRSPA 60

QY 61 GQLVVRPCPAFFYGVRYNTTNGYRECLANGSWAARVNYSECOEILNEEKSKVHYHVAV 120

DB 61 GQLVVRPCPAFFYGVRYNTTNGYRECLANGSWAARVNYSECOEILNEEKSKVHYHVAV 120

QY 121 IINYLGHCSLVALLVAFVLFLRLPGCTHWGDQADGALVGPWPGAPQVRRSTRCLR 180

DB 121 IINYLGHCSLVALLVAFVLFLRLPGCTHWGDQADGALVGPWPGAPQVRRSTRCLR 180

QY 181 NIHNWNLISAFILRNATFVVLQVTSPEVHQSVNGWCRLVTAAYNYFHVTFNPFMFGEGC 240

DB 152 NIHNWNLISAFILRNATFVVLQVTSPEVHQSVNGWCRLVTAAYNYFHVTFNPFMFGEGC 211

QY 241 YLHTAIVLTYSTDLRKWMFICIGWGPVPIIIVAMAIGKLYYDNEKCFKRPVGYTDYI 300

DB 212 YLHTAIVLTYSTDLRKWMFICIGWGPVPIIIVAMAIGKLYYDNEKCFKRPVGYTDYI 271

QY 301 YQGPMLVLLINFIPLFNIVRIIMTKLRASSTSETIYQKAVKATLVLLPLGITVMLPFF 360

DB 272 YQGPMLVLLINFIPLFNIVRIIMTKLRASSTSETIYQKAVKATLVLLPLGITVMLPFF 331

QY 361 VNPGEDEVSRVFIYFNSFLESFQGFVSVFYCFNLSEVRSAIRKRWHRWQDKHSIRARV 420

DB 332 VNPGEDEVSRVFIYFNSFLESFQGFVSVFYCFNLSEVRSAIRKRWHRWQDKHSIRARV 391

QY 421 ARAMSIPTSPTRVSPHSIKQSTAV 444

DB 392 ARAMSIPTSPTRVSPHSIKQSTAV 415

## RESULT 13

US-10-649-852-4

; Sequence 4, Application US/10649852

; Publication No. US20040101911A1

; GENERAL INFORMATION:

; APPLICANT: The Procter & Gamble Company

; APPLICANT: Isfort, Robert

; APPLICANT: Sheldon, Russell

; TITLE OF INVENTION: Methods for Identifying Compounds for Regulating Muscle Mass or F

; TITLE OF INVENTION: Using Corticotropin Releasing Factor Receptors



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; FILE REFERENCE: 8448R
; CURRENT APPLICATION NUMBER: US/10/649,852
; PRIOR FILING DATE: 2003-08-27
; PRIOR APPLICATION NUMBER: US 09/799,378
; PRIOR FILING DATE: 2001-03-06
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 415
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-649-852-4

Query Match          91.8%; Score 2186.5; DB 4; Length 415;
Best Local Similarity 93.5%; Pred. No. 5e-199;
Matches 415; Conservative 0; Mismatches 0; Indels 29; Gaps 1;

QY 1 MCGHPQLRLVKALLLGLNPNVSASLQDQHCESLSLASNISGLQCNASVDLIGTCWPRSPA 60
DB 1 MCGHPQLRLVKALLLGLNPNVSASLQDQHCESLSLASNISGLQCNASVDLIGTCWPRSPA 60
QY 61 GOLVVRPCPAFFYGVRYNTNNGYRECLANGSWAARVNYSECQEIINNEEKKSKVHYHVA 120
DB 61 GOLVVRPCPAFFYGVRYNTNNGYRECLANGSWAARVNYSECQEIINNEEKKSKVHYHVA 120
QY 121 IINYLGHCSLSVALLVAFVLFLRLRPGCTHWGDAQDALEVGAPWSGAPFQVRRSTRCLR 180
DB 121 IINYLGHCSLSVALLVAFVLFLRLRPGCTHWGDAQDALEVGAPWSGAPFQVRRSTRCLR 180
QY 181 NIHNWNLISAFILRNATFVQLTMSPEVHQSNGWCRVLTAAYNYFHVNTNPFMMFEGGC 240
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QY 241 YLHTAIVLTYSTDRLRKWMFICIGWGPPIIIVAMAIGKLYYDNEKCFKRGPGVYTDYI 300
DB 212 YLHTAIVLTYSTDRLRKWMFICIGWGPPIIIVAMAIGKLYYDNEKCFKRGPGVYTDYI 271
QY 301 YQGPMLVLLINFIPLFNIVRIILMTKLRASTTSETIYQYKAVKATVLLPLGITMPLFF 360
DB 272 YQGPMLVLLINFIPLFNIVRIILMTKLRASTTSETIYQYKAVKATVLLPLGITMPLFF 331
QY 361 VNPGEDEVSRVVIYFNSFLESFQGFVSVFYCFNLSEVRSAIRKWHRWQDKHSIRARV 420
DB 332 VNPGEDEVSRVVIYFNSFLESFQGFVSVFYCFNLSEVRSAIRKWHRWQDKHSIRARV 391
QY 421 ARAMSIPTSPTRVSHSIKQSTAV 444
DB 392 ARAMSIPTSPTRVSHSIKQSTAV 415

RESULT 15
US-09-826-509-483
; Sequence 483, Application US/09826509
; Publication No. US20030204073A1
; GENERAL INFORMATION:
; APPLICANT: Lehmann-Bruinsma, Karin
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lin, I-lin
; TITLE OF INVENTION: No. US20030204073A1-Endogenous, Constitutively Activated Known G
; FILE REFERENCE: AREN-207
; CURRENT APPLICATION NUMBER: US/09/826,509
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/195,747
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 589
; SOFTWARE: PatentIn Version 2.1
; SEQ ID NO 483
; LENGTH: 415
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-826-509-483

Query Match          91.6%; Score 2180.5; DB 3; Length 415;
Best Local Similarity 93.2%; Pred. No. 1.9e-198;
Matches 414; Conservative 0; Mismatches 1; Indels 29; Gaps 1;

QY 1 MCGHPQLRLVKALLLGLNPNVSASLQDQHCESLSLASNISGLQCNASVDLIGTCWPRSPA 60
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QY 121 IINYLGHCSLSVALLVAFVLFLRLRPGCTHWGDAQDALEVGAPWSGAPFQVRRSTRCLR 180
DB 121 IINYLGHCSLSVALLVAFVLFLRLRPGCTHWGDAQDALEVGAPWSGAPFQVRRSTRCLR 180
QY 181 NIHNWNLISAFILRNATFVQLTMSPEVHQSNGWCRVLTAAYNYFHVNTNPFMMFEGGC 240
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QY 241 YLHTAIVLTYSTDRLRKWMFICIGWGPPIIIVAMAIGKLYYDNEKCFKRGPGVYTDYI 300
DB 212 YLHTAIVLTYSTDRLRKWMFICIGWGPPIIIVAMAIGKLYYDNEKCFKRGPGVYTDYI 271
QY 301 YQGPMLVLLINFIPLFNIVRIILMTKLRASTTSETIYQYKAVKATVLLPLGITMPLFF 360
DB 272 YQGPMLVLLINFIPLFNIVRIILMTKLRASTTSETIYQYKAVKATVLLPLGITMPLFF 331
QY 361 VNPGEDEVSRVVIYFNSFLESFQGFVSVFYCFNLSEVRSAIRKWHRWQDKHSIRARV 420
DB 332 VNPGEDEVSRVVIYFNSFLESFQGFVSVFYCFNLSEVRSAIRKWHRWQDKHSIRARV 391
QY 421 ARAMSIPTSPTRVSHSIKQSTAV 444
DB 392 ARAMSIPTSPTRVSHSIKQSTAV 415

RESULT 14
US-10-450-097-14
; Sequence 14, Application US/10450097
; Publication No. US20040110252A1
; GENERAL INFORMATION:
; APPLICANT: Septegen Ltd
; TITLE OF INVENTION: Yeast-Based Assay
; FILE REFERENCE: DE/p/01948PCT
; CURRENT APPLICATION NUMBER: US/10/450,097
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: GB 0030038.4
; PRIOR FILING DATE: 2000-12-08
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 415
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-450-097-14

Query Match          91.8%; Score 2186.5; DB 4; Length 415;
Best Local Similarity 93.5%; Pred. No. 5e-199;
Matches 415; Conservative 0; Mismatches 0; Indels 29; Gaps 1;
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Db 121 IINYLGHICISLVALVAFVLFLRL-----RSIRCLR 151
QY 181 NIITHMLISAFILRNATWVVQLTMSPEVHQSNVGCRLVTAAYNYFHVNTNPFMMFEGC 240
Db 152 NIITHMLISAFILRNATWVVQLTMSPEVHQSNVGCRLVTAAYNYFHVNTNPFMMFEGC 211
QY 241 YLHTAIVLTYSTDRLRKWMFICIGWGVPPPIIVAMAIGKLYYDNEKCWFGRPGVYTDYI 300
Db 212 YLHTAIVLTYSTDRLRKWMFICIGWGVPPPIIVAMAIGKLYYDNEKCWFGRPGVYTDYI 271
QY 301 YQGPMLVLLINFIFLNIIVRIILMTKLRASTTSETIOYRKAVKATVLLPLLGITTMLFF 360
Db 272 YQGPMLVLLINFIFLNIIVRIILMTKLRASTTSETIOYRKAVKAPVLLPLLGITTMLFF 331
QY 361 VNPGEDEVSRVVFIIYFNSPLESPQGFVSVFYCFLNSEVRSAIRKWHRWQDKHSIRARV 420
Db 332 VNPGEDEVSRVVFIIYFNSPLESPQGFVSVFYCFLNSEVRSAIRKWHRWQDKHSIRARV 391
QY 421 ARAMSIPTSPTRVSPHSHIKQSTAV 444
Db 392 ARAMSIPTSPTRVSPHSHIKQSTAV 415
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Search completed: March 16, 2006, 17:24:47  
Job time : 170 secs

GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 16, 2006, 17:22:09 ; Search time 22 Seconds  
(without alignments)  
577.662 Million cell updates/sec

Title: US-10-649-193-15  
Perfect score: 2381  
Sequence: 1 MGHQPQLRVKALLLLGLNP.....SIPTSPTRVFSHKQSTAV 444

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 169630 seqs, 28622889 residues

Total number of hits satisfying chosen parameters: 169630

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA New.\*  
1: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB\_PEP.\*  
2: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB\_PEP.\*  
3: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB\_PEP.\*  
4: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB\_PEP.\*  
5: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB\_PEP.\*  
6: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB\_PEP.\*  
7: /cgn2\_6/ptodata/2/pubpaa/US11\_NEW\_PUB\_PEP.\*  
8: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB\_PEP.\*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	498.5	20.9	273	7	US-11-206-587-34
2	478	20.1	463	6	US-10-501-411A-341
3	459.5	19.3	438	7	US-11-090-439-29
4	459.5	19.3	438	7	US-11-090-439-31
5	209	8.8	910	7	US-11-206-587-17
6	207.5	8.7	742	7	US-11-127-877-43
7	207.5	8.7	765	6	US-10-821-234-1164
8	205	8.6	690	6	US-10-131-826A-306
9	205	8.6	690	6	US-10-973-115B-306
10	189.5	8.0	797	7	US-11-241-956-4
11	182	7.6	693	6	US-10-131-826A-406
12	182	7.6	693	6	US-10-973-115B-406
13	166	7.0	549	7	US-11-241-956-7
14	165	6.9	2923	7	US-11-200-822-3
15	163	6.8	578	7	US-11-241-956-2
16	156.5	6.6	565	7	US-11-080-991-100
17	98.5	4.1	380	6	US-10-330-773-443
18	98.5	4.1	920	7	US-11-027-512-2574
19	97.5	4.1	400	7	US-11-096-568A-7537
20	97.5	4.1	419	7	US-11-067-884-8
21	97.5	4.1	432	7	US-11-087-099-4608
22	97.5	4.1	432	7	US-11-096-568A-7536
23	97	4.1	342	7	US-11-174-751-19
24	97	4.1	358	6	US-10-055-877-177
25	94.5	4.0	358	7	US-11-174-819-17

26	93.5	3.9	432	7	US-11-087-099-367	Sequence 367, App
27	93.5	3.9	434	7	US-11-087-099-8116	Sequence 8116, Ap
28	92.5	3.9	358	7	US-11-174-816-52	Sequence 52, Appl
29	92.5	3.9	358	7	US-11-174-819-24	Sequence 24, Appl
30	92	3.9	337	7	US-11-174-816-43	Sequence 43, Appl
31	92	3.9	337	7	US-11-174-819-11	Sequence 11, Appl
32	92	3.9	342	7	US-11-087-099-2365	Sequence 2365, Ap
33	92	3.9	489	7	US-11-087-099-9063	Sequence 9063, Ap
34	91	3.8	358	7	US-11-174-816-68	Sequence 68, Appl
35	91	3.8	358	7	US-11-174-819-87	Sequence 87, Appl
36	90.5	3.8	267	7	US-11-098-686-10146	Sequence 10146, A
37	89.5	3.8	401	7	US-11-096-568A-25197	Sequence 25197, A
38	89.5	3.8	419	7	US-11-096-568A-25196	Sequence 25196, A
39	89.5	3.8	433	7	US-11-087-099-567	Sequence 567, App
40	89.5	3.8	450	7	US-11-096-568A-25195	Sequence 25195, A
41	89	3.7	337	7	US-11-174-816-58	Sequence 58, Appl
42	89	3.7	424	7	US-11-090-439-5	Sequence 5, Appl
43	88.5	3.7	412	7	US-11-170-153-4	Sequence 4, Appl
44	88.5	3.7	412	7	US-11-170-166-4	Sequence 4, Appl
45	88.5	3.7	412	7	US-11-170-351-4	Sequence 4, Appl

ALIGNMENTS

RESULT 1

US-11-206-587-34  
; Sequence 34, Application US/11206587  
; Publication No. US20060040306A1  
; GENERAL INFORMATION:  
; APPLICANT: Leiby, Kevin R.  
; APPLICANT: Kapeller-Libermann, Rosana  
; APPLICANT: Glucksmann, Maria A.  
; TITLE OF INVENTION: 38650, 28472, 5495, 65507, 81588, AND  
; TITLE OF INVENTION: 14354 METHODS AND COMPOSITIONS OF HUMAN PROTEINS AND USES  
; TITLE OF INVENTION: THEREOF  
; FILE REFERENCE: 381552004900  
; CURRENT APPLICATION NUMBER: US/11/206,587  
; CURRENT FILING DATE: 2005-08-18  
; PRIOR APPLICATION NUMBER: US/10/012,140  
; PRIOR FILING DATE: 2001-11-08  
; PRIOR APPLICATION NUMBER: 60/246,768  
; PRIOR FILING DATE: 2000-11-08  
; PRIOR APPLICATION NUMBER: 60/246,772  
; PRIOR FILING DATE: 2000-11-08  
; PRIOR APPLICATION NUMBER: 60/249,185  
; PRIOR FILING DATE: 2000-11-15  
; NUMBER OF SEQ ID NOS: 49  
; SOFTWARE: PastSeq for Windows Version 4.0  
; SEQ ID NO 34  
; LENGTH: 273  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Consensus amino acid sequence  
US-11-206-587-34

Query Match 20.9%; Score 498.5; DB 7; Length 273;  
Best Local Similarity 38.7%; Pred. No. 9.5e-39;  
Matches 118; Conservative 45; Mismatches 79; Indels 63; Gaps 11;

QY	121	IINVLGHC	SLVALLVAFVFLRLRPGCTHGWGDQDALEVGAPWGAPQVRSIRCL	179
Db	6	VIVTVGYSL	SSLLVCLLAIATFL	36
QY	180	RNIHWNLSA	FILRNATFVQLTSPSEVHQSNVGCRLVTAAYNYFHTNPFWMFEGEG	239
Db	37	RNIHWNLF	FUSFILRNALSFLIGDAVL	89
QY	240	CYLHRTAIVLT	---YSTDRLEKWMFICIGWGVPPPIIIVAWAI	284
Db	90	LXLYTLVTVT	VEFFSERKELWVLLIGWGVPAVFTVIMAI	149

QY 285 EK-CWFGKRGVYDYIYQGMILVLLINFLFNIVRILMTKLRAST-----TSETIQYR 339  
Db 150 EGCWLSNDTNSGFWMIKGPILLIILVFIPIFNILRIILVQKLRIIDSLSPQGETDQYR 209  
QY 340 K--AVKATVLLPLGLTYMLFFVNPGEDE---VSRVVFYFNSFLSFQGFVSVFYCF 394  
Db 210 KGLRVKSTLLPLGLTWILFLFAP-EDQSQGLSLVFLYFLIILNSPQGFVAVLYCF 268  
QY 395 LNSEV 399  
Db 269 LNSEV 273

RESULT 2  
US-10-501-411A-341  
; Sequence 341, Application US/10501411A  
; Publication No. US20050014678A1  
; GENERAL INFORMATION:  
; APPLICANT: Cowley, Michael  
; APPLICANT: Cone, Roger  
; APPLICANT: Low, Malcolm  
; APPLICANT: Bulter, Andrew  
; APPLICANT: Bloom, Stephen Robert  
; APPLICANT: Small, Caroline Jane  
; APPLICANT: Batterham, Rachel Louise  
; APPLICANT: Ghatel, Mohammad Ali  
; TITLE OF INVENTION: Modification of Feeding Behavior Using PYY and GLP-1  
; FILE REFERENCE: AI 9248US  
; CURRENT APPLICATION NUMBER: US/10/501.411A  
; CURRENT FILING DATE: 2004-07-12  
; PRIOR APPLICATION NUMBER: PCT/GB03/00062  
; PRIOR FILING DATE: 2003-01-10  
; PRIOR APPLICATION NUMBER: PCT/US02/31944  
; PRIOR FILING DATE: 2002-09-24  
; PRIOR APPLICATION NUMBER: 60/392,109  
; PRIOR FILING DATE: 2002-06-28  
; PRIOR APPLICATION NUMBER: GB 0200507.2  
; PRIOR FILING DATE: 2002-01-10  
; NUMBER OF SEQ ID NOS: 341  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 341  
; LENGTH: 463  
; TYPE: PRT  
; ORGANISM: homo sapiens  
US-10-501-411A-341

Query Match 20.1%; Score 478; DB 6; Length 463;  
Best Local Similarity 28.7%; Pred. No. 1.4e-36;  
Matches 139; Conservative 74; Mismatches 172; Indels 100; Gaps 20;

QY 1 MCGHP-QLRVKAALLGL-----NPVSASLQ-----DQHCBSLSLASN---I 39  
Db 1 MAGAPGLRL--ALLLLGMVGRAGPRPQGGATVSLMTVQKRYRQCQR-SLTEDPPPPA 57  
QY 40 SGIQCNASVDLIGTCWPRSPAGQVLRPCPAPFYGVRYNTNNGYRECLANGSWAARVN- 98  
Db 58 TDLFCNRTFDEY-ACHFDGEPGSFVNVSCDWYLPWASSVPGQHVYFCTAGLWQKDNS 116  
QY 99 -----YSEQEILNEKSKVHYHVAVINY-LGHCISLVALLVAPVFLRLRPOCTHW 151  
Db 117 SLPRDLSECESKRGSSPERQLFLYIITVGVYALSPSALVIASAILLGF----- 169  
QY 152 GQADGALEVGAPWPGAPQVRSISCLRNIIHNLISAFILRNATWVVVQLTM----- 205  
Db 170 -----RHLHCTRNIIHNLISAFILRNATWVVVQLTM----- 207  
QY 206 SPEVHQSNGW-----CRLVTAAYNYFHTNFFMMFGCGCYLHTAIVLTYSTDR 254  
Db 208 AAQHQH----WDGLLSYQDSLSCLRVLLMQYCVAAANYWLLAVEGYLYLTLLAFVSFE- 262  
QY 255 LRKWF-----ICITGWGPPFIIVAWAKLYYDNEKWFGRKPGVYTDYIYQGMILVLLI 311  
Db 263 --QWIFRLYVSGWGPVLLFVVPWGIKVLVEDEGCW--TRNSNMNYWLIIRLPIFPAIGV 319

QY 312 NFIFLFIIVRILMTKLRASTSETIQYRKAVKATVLLPLGLITYMLF-FVNPGEDEVSR 370  
Db 320 NFIFVVRVICIVSVKUKANLMCKTDIKCLRAKSTLLIPLLGTHFVIFAPV---MDEHAR 376  
QY 371 VVFYFNSFLE-----SFQGFVSVFYCFNLSEVRSAIRKWRHW---QDKHSIRARVARAM 424  
Db 377 GTLRFIKLFTLSFTSFQGLWVAILYCFVNVVQLEFRKSWERWRLHHLHQDSSMKPL 436  
QY 425 SIPTS 429  
Db 437 KCPTS 441

RESULT 3  
US-11-090-439-29  
; Sequence 29, Application US/11090439  
; Publication No. US20050266442A1  
; GENERAL INFORMATION:  
; APPLICANT: Squillace, Rachel  
; APPLICANT: Weiner, Michael P.  
; TITLE OF INVENTION: Immortalized Human Tuberos Sclerosis Null  
; FILE REFERENCE: 24318-502  
; CURRENT APPLICATION NUMBER: US/11/090,439  
; CURRENT FILING DATE: 2005-03-25  
; PRIOR APPLICATION NUMBER: 60/556,344  
; PRIOR FILING DATE: 2004-03-25  
; NUMBER OF SEQ ID NOS: 62  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 29  
; LENGTH: 438  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-090-439-29

Query Match 19.3%; Score 459.5; DB 7; Length 438;  
Best Local Similarity 28.2%; Pred. No. 6.8e-35;  
Matches 118; Conservative 75; Mismatches 161; Indels 65; Gaps 13;

QY 4 HPQLRLVKALLLLGLNPVSAISLQDQHCESLSLASNISGLQCNASVDLIGTCWPRSPAGQL 63  
Db 22 HPECRF-----HLEIQEETKCAELLRSQTEKHKACSGVWDNI--TCWRPANVGET 70  
QY 64 VVRPCPAPFYGVRYNTNNGYRECLANGSWAARVNYSQEQEILNEKSKVHYHVAVIN 123  
Db 71 VTPCPKVFESNF-YSKAGNISKNCTSDGWSSETFPDFVDACGYSDPEDESKITFYIILVKAI 129  
QY 124 Y-LGHCISLVALLVAPVFLRLRPGCTHWGDDQADGALEVGAPWPGAPQVRSISCLRNII 182  
Db 130 YTLGYSVLSLMTSGIIL-----C-----LFRKLHCTRNY 160  
QY 183 IHNLISAFILRNATWVVVQLTMSPEVHQSNGV-----W--CRLVTAAYNYFHTV 230  
Db 161 IHLNLFSLFILR-----AISVLKDDVLYSSSTGLHCPDPSPSSWGCKLSLFLQYCINA 215  
QY 231 NFFWMPGECYLTALVTYSTDRLRKWNFICIGWGVPPPIIVANAIGKLYDNEKWF 290  
Db 216 NPFLLVEGLYLTLLVAMLPARRC-FLAYLLIGMGLPTVCIGAMTAARLYLEDTCMDT 274  
QY 291 KRPGVYTDYIYQGMILVLLINFLFNIVRILMTKLRASTT--SETIQYRKAVKATVLL 348  
Db 275 NDHSV-PWVIRIPILISIIIVNFVLFISIIRILLQKLTSPDVGNDQSQYKRLAKSTLLL 333  
QY 349 LPPLGLTYMLFFVNPGEDEVSRVVFYFNSFLSFQGFVSVFYCFNLSEVRSAIRKRW 407  
Db 334 IPLFGVHYNVFAVFP--ISISSKYQLFELCLGSGFGLVAVLYCYFLNSEVQCELRKW 390

RESULT 4  
US-11-090-439-31  
; Sequence 31, Application US/11090439  
; Publication No. US20050266442A1

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; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 910
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-206-587-17

Query Match      8.8%; Score 209; DB 7; Length 910;
Best Local Similarity 23.4%; Pred. No. 2.7e-11;
Matches 74; Conservative 62; Mismatches 122; Indels 58; Gaps 14;

QY 122 INVLGHCSISVALLVAFV--LFLRLRPGCTHGGDQADGALEVGAPWSGAPFQVRRS-IR 177
DB 588 ITVVGIGISGSIUCLCLITALEF-----WK-----QIKKSQTS 620

QY 178 CLRNIIHWNLIISAFILRNATVFFVQVLTMSPEVHQSNVGCRLVTAAYNYEHVTNFFVMFG 237
DB 621 HTRRICWNIALSLLIAD-VVFIVGATVDTVPNSGV--CTAAVFFTHFFVLSLFFWMLM 677

QY 238 EGCYLHTAIVLY--STDRLRKWMFTICIGMVGVPPI-IVAWAI---GKLYVDNEKCKWFGK 291
DB 678 LGILLAYRIILVFHMAQHLMAVAGCLGCGCLIIISVITIAVTPSNTYKRRKDVCLWLNW 737

QY 292 RGVYTDYIQGPMLVLLNIFLFLNIVRLMTKLRASVTSITQ-----YKAVKAT 345
DB 738 SNGGKPLFAVPVPAALIAVNFV---VLLVLTKLWRPTVGBRLSRDDKATIIRVGSL 793

QY 346 LVLLPLLGITYMLFVFNPGDEVSRRVFIYFNSPLESFQGFVFSVFCFLNSEVRSAIRK 405
DB 794 LIITPLGLTWG-FGIGTIVDSQNLAWHVF-ALLNAFQGFILCFGLILDSKLRQLLEN 851

QY 406 R-----WHRWDQKHS 415
DB 852 KLSALSSWKQTEKQNS 867

RESULT 6
US-11-127-877-43
; Sequence 43, Application US/11127877
; Publication No. US20050287565A1
; GENERAL INFORMATION:
; APPLICANT: Merckhiers, Pascal G.
; APPLICANT: Hoffmann, Marcel
; APPLICANT: Spittaels, Koenraad F. F.
; APPLICANT: Laenen, Wendy
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
; TITLE OF INVENTION: Amyloid-Beta Protein Production
; FILE REFERENCE: F27,800-B USA
; CURRENT APPLICATION NUMBER: US/11/127,877
; CURRENT FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: 60/570,352
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/603,948
; PRIOR FILING DATE: 2004-08-24
; NUMBER OF SEQ ID NOS: 590
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 43
; LENGTH: 742
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-127-877-43

Query Match      8.7%; Score 207.5; DB 7; Length 742;
Best Local Similarity 26.9%; Pred. No. 3e-11;
Matches 89; Conservative 51; Mismatches 128; Indels 63; Gaps 18;

QY 90 NGSWAARVNYSEQEILNEBKSKSVHYH-----AVIINYLGHCISLVALLVAFVFLRLR 145
DB 427 NGSTTCQCSHLSFAIL-----MAHYDVEDWKLTITRVGLALSFLCILLCILTLFLVR 480

QY 146 PGCTHGGDQADGALEVGAPWSGAPFQVRRSIRCURNIIHWNL-ISAFILRNATVFFVQVLT 204

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Db 481 P-----IQSRTTIHLHCICLVF--GSTIFLAGI- 508  
QY 205 MSPEVHQSNGM--CRLVTAAYNYFHTNPFMMFEGCYLHTAIVLYSTDR-L-RKMFIC 262  
Db 509 ---ENEGGQGLRCRLVAGLLHYCFLLAFCWMSLEGLYFLVVRVFOQGLSTRWLCL- 564  
QY 263 IGMGVPPPII-VAMAI--GKLYDNEKCMFGKRGVVDYIYQGPMLVLLIN-FIFLNI 319  
Db 565 IGVGPVLLIVGSAIYSKGYGRPCWLDFOGFLWSFL--GPVTFILCNVAVFTTV 622  
QY 320 VRILMTKLRASTTSETIQRKAVKATLVL-LPLLGYTM--LFFVNPGEDEVSRVFIYP 376  
Db 623 WKLTQKFSINPDMMKKLKRALTITAIQLFLGCTWVGLFIF---DDRS-LVLTIV 677  
QY 377 NSPLESFOGFFVSVCFLNSEVRSIRKRW 407  
Db 678 FTILNCLOGAFLYLHCLLNKKVREYRK-W 707

## RESULT 7

US-10-821-234-1164  
; Sequence 1164, Application US/10821234  
; Publication No. US20050255114A1  
; GENERAL INFORMATION:  
; APPLICANT: Labat, Ivan  
; APPLICANT: Stache-Crain, Birgit  
; APPLICANT: Tang, Y. Tom  
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia  
; FILE REFERENCE: 821A  
; CURRENT APPLICATION NUMBER: US/10/821,234  
; PRIOR FILING DATE: 2004-04-07  
; PRIOR APPLICATION NUMBER: US 60/462,047  
; PRIOR FILING DATE: 2003-04-07  
; NUMBER OF SEQ ID NOS: 1704  
; SOFTWARE: pt\_seq\_genes Version 1.0  
; SEQ ID NO 1164  
; LENGTH: 765  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-821-234-1164

Query Match 8.7%; Score 207.5; DB 6; Length 765;  
Best Local Similarity 26.9%; Pred. No. 3.1e-11;  
Matches 89; Conservative 51; Mismatches 128; Indels 63; Gaps 18;

QY 90 NGSWAARVNSYECQEIINBEKSKVHYV-----AVIINYLGHICISLVALLVAFVFLRLR 145  
Db 450 NGSTTCQCSHLSSFAIL-----MAHYDVEDMKLTITRVGLALSFLCLLCILTELLVR 503  
QY 146 PGCTHWGDQADGALEVGAPWPGAPFQVRSIRCLRNIIHNL-ISAFLRNATWFWVQLT 204  
Db 504 P-----IQSRTTIHLHCICLVF--GSTIFLAGI- 531  
QY 205 MSPEVHQSNGM--CRLVTAAYNYFHTNPFMMFEGCYLHTAIVLYSTDR-L-RKMFIC 262  
Db 532 ---ENEGGQGLRCRLVAGLLHYCFLLAFCWMSLEGLYFLVVRVFOQGLSTRWLCL- 587  
QY 263 IGMGVPPPII-VAMAI--GKLYDNEKCMFGKRGVVDYIYQGPMLVLLIN-FIFLNI 319  
Db 588 IGVGPVLLIVGSAIYSKGYGRPCWLDFOGFLWSFL--GPVTFILCNVAVFTTV 645  
QY 320 VRILMTKLRASTTSETIQRKAVKATLVL-LPLLGYTM--LFFVNPGEDEVSRVFIYP 376  
Db 646 WKLTQKFSINPDMMKKLKRALTITAIQLFLGCTWVGLFIF---DDRS-LVLTIV 700  
QY 377 NSPLESFOGFFVSVCFLNSEVRSIRKRW 407  
Db 701 FTILNCLOGAFLYLHCLLNKKVREYRK-W 730

## RESULT 8

US-10-131-826A-306

; Sequence 306, Application US/10131826A  
; Publication No. US20050245730A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Beresini, Maureen  
; APPLICANT: DeForge, Laura  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Sherwood, Steven  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K  
; APPLICANT: Wood, William  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P3330RIC128  
; CURRENT APPLICATION NUMBER: US/10/131,826A  
; CURRENT FILING DATE: 2002-04-24  
; PRIOR APPLICATION NUMBER: 60/049911  
; PRIOR FILING DATE: 1997-06-18  
; PRIOR APPLICATION NUMBER: 60/056974  
; PRIOR FILING DATE: 1997-08-26  
; PRIOR APPLICATION NUMBER: 60/059113  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/059115  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/059117  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/059122  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/059184  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/059263  
; PRIOR FILING DATE: 1997-09-18  
; PRIOR APPLICATION NUMBER: 60/059352  
; PRIOR FILING DATE: 1997-09-19  
; PRIOR APPLICATION NUMBER: 60/059588  
; PRIOR FILING DATE: 1997-09-19  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; SEQ ID NO 306  
; NUMBER OF SEQ ID NOS: 550  
; LENGTH: 690  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-10-131-826A-306

Query Match 8.6%; Score 205; DB 6; Length 690;  
Best Local Similarity 23.2%; Pred. No. 4.7e-11;  
Matches 86; Conservative 54; Mismatches 135; Indels 96; Gaps 17;  
QY 73 YGVRYNTNNGVRECLA-----NGSWAA---RVNSYECQEIINBEKKS-----KVH 115  
Db 355 FTLSHRKVTDRYRSLCAFWNSPDTMNGSWSEGCBLTYS-----NETHTSCRCNHLTH 408  
QY 116 -----YHVAIINYLGHICISLVALLVAFVFLRLRPGCTHWGDQADGALE 160  
Db 409 FAILSSGPSIGIKDYNILTRITQIILISLCIAICITP----- 449  
QY 161 VGAPSGAPFQVRSIRCLRNIIHNLISAFILRNATWFWVQLTMSPEVHQSNGVRCRLV 220  
Db 450 -----WFFS-----BIQSTRFTIHKNLCCSLFLAELVFLVGINT-----NTNKLFCSLI 493  
QY 221 TAAVNYFHTNPFMMFEGCYLHTAIV-LTYSTDRLRKMFICIGWGVPPPIV---AWA 276  
Db 494 AGLLHYFFLAAPANMCIEGIIHLIVGVGVYINKGFLHKNFYI---FGYLSPAVVVGFSAA 550

QY 277 IGKLYDNEK-CWFGKRPVYTDYIYOGPMILVLLNFIPLFNIVRILMTKLAESTTSET 335  
Db 551 LGVRYGTGTTKVCWLSTENNFIWFSFI--GPACLIILVN-LIAFGVLIYKVPFRHTAGLKPEV 607  
QY 336 IQY---RKAVKATLVLPLLGITY---MLFFVNPGEDESVRVVFIYFNSFLSFQGFVFS 389  
Db 608 SCFENIRSCARGALALLFLGTTWIFGVHLVH-----ASVVTAYLFTVSNAPQGMFIF 661  
QY 390 VFYCFNLSEVR 400  
Db 662 LFLCVLSRKIQ 672  
RESULT 9  
US-10-973-115B-306  
; Sequence 306, Application US/10973115B  
; Publication No. US20060040351A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Beresini, Maureen  
; APPLICANT: Deforge, Laura  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Sherwood, Steven  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ACIDS ENCODING  
; FILE REFERENCE: 39870-3330R1C300C1  
; CURRENT APPLICATION NUMBER: US/10/973,115B  
; CURRENT FILING DATE: 2004-10-22  
; PRIOR APPLICATION NUMBER: US 10/145,747  
; PRIOR FILING DATE: 2002-05-14  
; PRIOR APPLICATION NUMBER: US 10/028,072  
; PRIOR FILING DATE: 2001-12-19  
; PRIOR APPLICATION NUMBER: PCT/US00/32678  
; PRIOR FILING DATE: 2000-12-01  
; PRIOR APPLICATION NUMBER: US 09/581,742  
; PRIOR FILING DATE: 2000-06-16  
; PRIOR APPLICATION NUMBER: PCT/US00/05746  
; PRIOR FILING DATE: 2000-03-02  
; PRIOR APPLICATION NUMBER: US 60/135,736  
; PRIOR FILING DATE: 1999-05-25  
; PRIOR APPLICATION NUMBER: US 60/123,090  
; PRIOR FILING DATE: 1999-03-05  
; NUMBER OF SEQ ID NOS: 550  
; SEQ ID NO 306  
; LENGTH: 690  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-973-115B-306  
Query Match 8.6%; Score 205; DB 6; Length 690;  
Best Local Similarity 23.2%; Pred. No. 4.7e-11;  
Matches 86; Conservative 54; Mismatches 135; Indels 96; Gaps 17;  
QY 73 YGVRYNTNNGYRECLA-----NGSWAA-----RVNSECQILNEKKGS-----KVH 115  
Db 355 FTLSHRKVTDRYSLCAFWNVSPDTMGNSWSEGCETYS-----NETHTSCRNHLTH 408  
QY 116 -----YHVAIIVNLHCISLIVALLVAVFLRLRPGCTHWGDAQDALE 160  
Db 409 FAILMSGSPSIGINDKYNILRITQIGIISLICIAICITFT----- 449

QY 161 VGAPSGAPFQVRRSIRCLRNIIHWNLIISAFILRNATFWVQLTMSPEVHQSNVGHCLRV 220  
Db 450 -----WFFS-----EQSTRTTIHKNLCCSLFLAELVFLVGINT-----NTNKLFCSII 493  
QY 221 TAAVNYFHTVNFPMFEGECYLHTAIV-LTYSIDRLRKWMFICIGWGVPPPIIV---AWA 276  
Db 494 AGLLHYFFLAAPAWMCIEGHLVLIUVGVYINNGFLHKFYI---FGYLSPAVVVGFSAA 550  
QY 277 IGKLYDNEK-CWFGKRPVYTDYIYOGPMILVLLNFIPLFNIVRILMTKLAESTTSET 335  
Db 551 LGVRYGTGTTKVCWLSTENNFIWFSFI--GPACLIILVN-LIAFGVLIYKVPFRHTAGLKPEV 607  
QY 336 IQY---RKAVKATLVLPLLGITY---MLFFVNPGEDESVRVVFIYFNSFLSFQGFVFS 389  
Db 608 SCFENIRSCARGALALLFLGTTWIFGVHLVH-----ASVVTAYLFTVSNAPQGMFIF 661  
QY 390 VFYCFNLSEVR 400  
Db 662 LFLCVLSRKIQ 672  
RESULT 10  
US-11-241-956-4  
; Sequence 4, Application US/11241956  
; Publication No. US20060024792A1  
; GENERAL INFORMATION:  
; APPLICANT: INCYTE GENOMICS INC.; BAUGHN, Mariah R.;  
; APPLICANT: GANDHI, Ameena R.; CHAWLA, Navinder K.;  
; APPLICANT: RAMKUMAR, Jayalaxmi; TRIBOULEY, Catherine M.;  
; APPLICANT: THORNTON, Michael B.; KALLICK, Deborah A.;  
; APPLICANT: YAO, Monique G.; ELLIOTT, Vicki S.;  
; APPLICANT: BURFORD, Neil; KHAN, Farrah A.;  
; APPLICANT: YUE, Henry; LU, Yan;  
; APPLICANT: ARVIZU, Chandra S.; ROOPA, Reddy M.;  
; APPLICANT: NGUYEN, Daniel B.; LEE, Ernestine A.;  
; APPLICANT: LU, Dying Aina M.; ISON, Craig H.;  
; APPLICANT: WALSH, Roderick T.; POLICKY, Jennifer L.  
; TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTORS  
; FILE REFERENCE: PI-0236 USN  
; CURRENT APPLICATION NUMBER: US/11/241,956  
; CURRENT FILING DATE: 2005-10-04  
; PRIOR APPLICATION NUMBER: US/10/398,036  
; PRIOR FILING DATE: 2003-03-28  
; PRIOR APPLICATION NUMBER: PCT/US01/30661  
; PRIOR FILING DATE: 2001-09-28  
; PRIOR APPLICATION NUMBER: US 60/245,855  
; PRIOR FILING DATE: 2000-11-03  
; PRIOR APPLICATION NUMBER: US 60/242,322  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: US 60/240,589  
; PRIOR FILING DATE: 2000-10-13  
; PRIOR APPLICATION NUMBER: US 60/249,343  
; PRIOR FILING DATE: 2000-11-15  
; PRIOR APPLICATION NUMBER: US 60/247,587  
; PRIOR FILING DATE: 2000-11-09  
; PRIOR APPLICATION NUMBER: US 60/245,900  
; PRIOR FILING DATE: 2000-11-03  
; PRIOR APPLICATION NUMBER: US 60/242,223  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: US 60/236,546  
; PRIOR FILING DATE: 2000-09-29  
; NUMBER OF SEQ ID NOS: 32  
; SOFTWARE: PERL Program  
; SEQ ID NO 4  
; LENGTH: 797  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; OTHER INFORMATION: Incyte ID No: 644692CD1  
US-11-241-956-4





APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ACIDS ENCODING  
FILE REFERENCE: 39870-3330301C300C1  
CURRENT APPLICATION NUMBER: US/10/973.115B  
CURRENT FILING DATE: 2004-10-22  
PRIOR APPLICATION NUMBER: US 10/145,747  
PRIOR FILING DATE: 2002-05-14  
PRIOR APPLICATION NUMBER: US 10/028,072  
PRIOR FILING DATE: 2001-12-19  
PRIOR APPLICATION NUMBER: PCT/US00/32678  
PRIOR FILING DATE: 2000-12-01  
PRIOR APPLICATION NUMBER: US 09/581,742  
PRIOR FILING DATE: 2000-06-16  
PRIOR APPLICATION NUMBER: PCT/US00/05746  
PRIOR FILING DATE: 2000-03-02  
PRIOR APPLICATION NUMBER: US 60/135,736  
PRIOR FILING DATE: 1999-05-25  
PRIOR APPLICATION NUMBER: US 60/123,090  
PRIOR FILING DATE: 1999-03-05  
NUMBER OF SEQ ID NOS: 550  
SEQ ID NO 406  
LENGTH: 693  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-973-115B-406

Query Match 7.6%; Score 182; DB 6; Length 693;  
Best Local Similarity 22.6%; Pred. No. 6.4e-09;  
Matches 83; Conservative 46; Mismatches 122; Indels 116; Gaps 14;

QY 91 GSWAARNVSECDEILNEEKSS-----KVHVHVAIINYLGHCHIS 130  
DB 359 GHSS-----AGCTVRRRTQSCFNHLTYFAVLWSSVEVDVHKHLYLSLVGCVWS 414  
QY 131 LVALLAVFLFLRLPGCTHGWQADGALVGPWSPQVRSIRCLRNIIHNNLISA 190  
DB 415 ALACLVTIAAYL-----C-----SRVPLPCRKRPRDYTIKVMNLLLA 452  
QY 191 FILRNATFWVQVLTMSPEVHQSNGVCLRVTAAYNFHVTNFWFMGEGCYLHTAIVL-- 248  
DB 453 VFLLDTSP-----LLSEVALTSGENGCSAIPHFSLILCLSNWGLEGNLRLVVEVF 508  
QY 249 -TVSTDLRLKRMFICIGWGPPIIIVAWAIGKLYDNEKCFKRGKPGVYTDYIYQGPML 307  
DB 509 GTVPGYLLK--LSAMGWG--FPIFLVTLVALVDVN-----YGPILL 547  
QY 308 VL-----LINFIFLN-----IVRILMTKLRASTTS 333  
DB 548 AVHRTPEGVTPSMCWIRDSLSVYITNLGLFLVFLFNMAMLATMVVQIIL--BLRPHT-- 603  
QY 334 ETIQYRKAVKATLVLLPLLGITVMLFPVNPGEDEVSRVVFYFNSFLESFQGFVSVFYC 393  
DB 604 ---QKSHVLTLLGLSLVLGLPWLALFPFSPASGTFFQLVV-LYLFSLITSFQGLFIPIWY 659  
QY 394 FLNSEVR 400  
DB 660 SMELQAR 666

RESULT 13  
US-11-241-956-7  
Sequence 7, Application US/11241956  
Publication No. US20060024792A1  
GENERAL INFORMATION:  
APPLICANT: INCITE GENOMICS INC.; BAUGHN, Mariah R.;  
APPLICANT: GRAUL Richard C.; CHAWLA, Narinder K.;  
APPLICANT: GANDHI, Ameena R.; HAFALIA, April J.A.;  
APPLICANT: RAMKUMAR, Javalaxmi; TRIBOULEY, Catherine M.;  
APPLICANT: THORNTON, Michael B.; KALLICK, Deborah A.;  
APPLICANT: YAO, Monique G.; ELLIOTT, Vicki S.;  
APPLICANT: BURFORD, Neil; KHAN, Farrah A.;  
APPLICANT: YUE, Henry; LU, Yan;

APPLICANT: ARVIZU, Chandra S.; ROOPA, Reddy M.;  
APPLICANT: NGUYEN, Danniell B.; LEE, Ernestine A.;  
APPLICANT: LU, Dyung Aina M.; ISON, Craig H.;  
APPLICANT: WALSH, Roderick T.; POLICKY, Jennifer L.  
TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTORS  
FILE REFERENCE: PI-0236 USN  
CURRENT APPLICATION NUMBER: US/11/241,956  
CURRENT FILING DATE: 2005-10-04  
PRIOR APPLICATION NUMBER: US/10/398,036  
PRIOR FILING DATE: 2003-03-28  
PRIOR APPLICATION NUMBER: PCT/US01/30661  
PRIOR FILING DATE: 2001-09-28  
PRIOR APPLICATION NUMBER: US 60/245,855  
PRIOR FILING DATE: 2000-11-03  
PRIOR APPLICATION NUMBER: US 60/242,322  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: US 60/240,589  
PRIOR FILING DATE: 2000-10-13  
PRIOR APPLICATION NUMBER: US 60/249,343  
PRIOR FILING DATE: 2000-11-15  
PRIOR APPLICATION NUMBER: US 60/247,587  
PRIOR FILING DATE: 2000-11-09  
PRIOR APPLICATION NUMBER: US 60/245,900  
PRIOR FILING DATE: 2000-11-03  
PRIOR APPLICATION NUMBER: US 60/242,223  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: US 60/236,546  
PRIOR FILING DATE: 2000-09-29  
NUMBER OF SEQ ID NOS: 32  
SOFTWARE: PERL Program  
SEQ ID NO 7  
LENGTH: 549  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc feature  
OTHER INFORMATION: Incyte ID No: 55012817CD1  
US-11-241-956-7

Query Match 7.0%; Score 166; DB 7; Length 549;  
Best Local Similarity 23.8%; Pred. No. 1.5e-07;  
Matches 72; Conservative 43; Mismatches 120; Indels 68; Gaps 12;

QY 117 HVAIINYLGHCHISLVALLVAVFLRLRPGCTHGWQADGALVGPWSPQVRSIRSI 176  
DB 266 HILTRISQAGCGVSMIFLAFTIILYAFRLSLRRFKSE-----DAP----- 306  
QY 177 RCLRNIIHNNLISAFILRNATFWVQVLTMSPEVHQSNGV-----WCLVTAAYNY 226  
DB 307 -----KIHVALGGSLLFLNLALFLV-----NVSGSGKSDAACWAR--GAVFHY 347  
QY 227 FHVTFNFWMPGEGCYLHTAIVLTYSTDLRLKMMFI-CIGMGVFPPIIVAWAIGLY---- 281  
DB 348 FLTCATWNGLEAFHLYLLAVRVNTYFGHYFLKLSLVGWLPAWLVIGTGSANSYGLYT 407  
QY 282 ---YDN-----EKWFGKRGVYTDYI-YQGPMLVLLINIFILFNIVRILMTKLRASTTS 333  
DB 408 IRDRENRTSLELCWFREGTMMVALYITVHGYYFLITFLFGMVVLAVVWKIFTLSRATAVK 467  
QY 334 ETIQYRKAVKATLVLLPLLGITVMLFPVNP-GEDEVSRVVFYFNSFLESFQGFVSVFY 392  
DB 468 ERGKRNKVLTLGLSLVLGLVGTWGLAIFTPLGLSTV--YIFALFN-----SLQGVFICWF 521  
QY 393 CFL 395  
DB 522 TIL 524

RESULT 14  
US-11-200-822-3  
Sequence 3, Application US/11200822  
Publication No. US20060040302A1  
GENERAL INFORMATION:  
APPLICANT: INCITE GENOMICS INC.; BAUGHN, Mariah R.;  
APPLICANT: GRAUL Richard C.; CHAWLA, Narinder K.;  
APPLICANT: GANDHI, Ameena R.; HAFALIA, April J.A.;  
APPLICANT: RAMKUMAR, Javalaxmi; TRIBOULEY, Catherine M.;  
APPLICANT: THORNTON, Michael B.; KALLICK, Deborah A.;  
APPLICANT: YAO, Monique G.; ELLIOTT, Vicki S.;  
APPLICANT: BURFORD, Neil; KHAN, Farrah A.;  
APPLICANT: YUE, Henry; LU, Yan;

```
/ APPLICANT: Bostein, et al.
/ TITLE OF INVENTION: Methods of Classifying, Diagnosing, Stratifying and
/ FILE REFERENCE: 2002850-0049
/ CURRENT APPLICATION NUMBER: US/11/200,822
/ CURRENT FILING DATE: 2005-08-10
/ NUMBER OF SEQ ID NOS: 15
/ SOFTWARE: Patent In Ver. 2.1
/ SEQ ID NO 3
/ LENGTH: 2923
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Cadherin EGF
/ OTHER INFORMATION: LAG Seven Pass G-Type Receptor 2
US-11-200-822-3

Query Match      6.9%; Score 165; DB 7; Length 2923;
Best Local Similarity 22.3%; Pred. No. 1.3e-06;
Matches 78; Conservative 64; Mismatches 113; Indels 94; Gaps 19;

QY 91 GSWAARVNTSECOELL-NEEKSKVHVHV---AVI-----INVLGHCHIS 130
Db 2332 GWSAR-----GCSVVRNESHVSCQCHMTSFAVLMDSRRENGEILPLKLTLYVALGVT 2387

QY 131 LVALLVAFVFLRLRPGCTHWGDAQDALEVGAPWSGAPPQVRRSIRCLRNIIHWNLISA 190
Db 2388 LAALLTLP-FFLT-----LRLRSNQH-----2410

QY 191 FILRN--ATWFFVQVLTSPVHNSGVN-CRLVTAAYNYFHVNFPMFGGCVLHTAI- 246
Db 2411 -IRNLTAALGLAQLVFLGQINQADLPFACTVAILLHFLYLCFTSWALLEALHLYRALT 2469

QY 247 -VLTGTDLRLKWMFCICGHPFPPIVAVAG---KLYYDNKCKWFGKRPVYTYI-- 300
Db 2470 EVRDVTGPMR--FYMLGWSVP-AFITGLAVLDPGEGYNDPCFWL-----SIYDTLWS 2522

QY 301 YQGPMLVLLINFIPLNIVRIILMTKLRASTTGETIQYK-----AVKATVLLPLLGIT 355
Db 2523 FAGVAFVMS-VFLY-----ILAAASCAQRQGFKKGVSGLOPSFAVLLLSAT 2575

QY 356 YMLFFVNPGBDESVRVVFIYFNFSFLSFQGFVSVFCFNLNSVRSAIR 404
Db 2576 WLLALLSVNSD---TLLFHLFCNCIQGPFIFLSYVLSKEVRKALK 2621

RESULT 15
US-11-241-956-2
/ Sequence 2, Application US/11241956
/ Publication No. US20060024792A1
/ GENERAL INFORMATION:
/ APPLICANT: INCYTE GENOMICS INC.; BAUGHN, Mariah R.;
/ APPLICANT: GAUL Richard C.; CHAWLA, Narinder K.;
/ APPLICANT: GANDHI, Aneena R.; HAFALIA, April J.A.;
/ APPLICANT: RAMKUMAR, Jayalaxmi; TRIBOULEY, Catherine M.;
/ APPLICANT: THORNTON, Michael B.; KALLICK, Deborah A.;
/ APPLICANT: YAO, Monique G.; ELLIOTT, Vicki S.;
/ APPLICANT: BURFORD, Neil; KHAN, Farrah A.;
/ APPLICANT: YUE, Henry; LU, Yan;
/ APPLICANT: ARVIZU, Chandra S.; ROOPA, Reddy M.;
/ APPLICANT: NGUYEN, Dannel B.; LEE, Ernestine A.;
/ APPLICANT: LU, Dyung Aina M.; ISON, Craig H.;
/ APPLICANT: WALSH, Roderick T.; POLICKY, Jennifer L.
/ TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTORS
/ FILE REFERENCE: FI-0236 USN
/ CURRENT APPLICATION NUMBER: US/11/241,956
/ CURRENT FILING DATE: 2005-10-04
/ PRIOR APPLICATION NUMBER: US/10/398,036
/ PRIOR FILING DATE: 2003-03-28
/ PRIOR APPLICATION NUMBER: PCT/US01/30661
/ PRIOR FILING DATE: 2001-09-28
/ PRIOR APPLICATION NUMBER: US 60/245,855
/ PRIOR FILING DATE: 2000-11-03
```

```
/ PRIOR APPLICATION NUMBER: US 60/242,322
/ PRIOR FILING DATE: 2000-10-20
/ PRIOR APPLICATION NUMBER: US 60/240,589
/ PRIOR FILING DATE: 2000-10-13
/ PRIOR APPLICATION NUMBER: US 60/249,343
/ PRIOR FILING DATE: 2000-11-15
/ PRIOR APPLICATION NUMBER: US 60/247,587
/ PRIOR FILING DATE: 2000-11-09
/ PRIOR APPLICATION NUMBER: US 60/245,900
/ PRIOR FILING DATE: 2000-11-03
/ PRIOR APPLICATION NUMBER: US 60/242,223
/ PRIOR FILING DATE: 2000-10-20
/ PRIOR APPLICATION NUMBER: US 60/236,546
/ PRIOR FILING DATE: 2000-09-29
/ NUMBER OF SEQ ID NOS: 32
/ SOFTWARE: PERL Program
/ SEQ ID NO 2
/ LENGTH: 578
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: misc feature
/ OTHER INFORMATION: Incyte ID No: 7477708CD1
US-11-241-956-2

Query Match      6.8%; Score 163; DB 7; Length 578;
Best Local Similarity 25.2%; Pred. No. 3e-07;
Matches 71; Conservative 51; Mismatches 108; Indels 52; Gaps 16;

QY 118 VAVIINYLGHCHISLVALLVAFVFLRLRPGCTHWGDAQDALEVGAPWSGAPPQVRRS-I 176
Db 315 ILTYITVVGIGISICSLILCL-----SIEV-LVMS---QVTKTEI 350

QY 177 RCLRNIIHWNLISAFILRNATWFFVQVLTMS-PEVHQSNVGVWCLVTAAYNYFHVNFPM 235
Db 351 TYLRHVCIYN-IAATLLMADVMFIVASFLSGPITHKG---CVAATFFVHFVFLSVFFWM 406

QY 236 FGGCVLHTAIVLTVSTDLRLKWMFC-----IGWGVPPPI-----IVAMAIGKLYYDNEKC 287
Db 407 LAKALLILYIMIVFHT--LPKSVLVASLPSVGYGCLAIATAITVAATFPGKGYLPEIC 464

QY 288 WFG-KRPGVYTDYIQGPMILVLLINFIPLNIVRIILMTKLRASTTSETIQYRKAV---- 342
Db 465 WLNWDMTKALLAFVI--PALAIVVN---LITVTVIVKTQRAAIGNSMFQEVRAIVRIS 519

QY 343 KATLVLLPLLGITYMLFPVNPGEDEVSRVVFYFNFSFLSFQ 384
Db 520 KNTAILTPLLGLTWG-FGVATVDDRSLAFHIF-SLLNAFQ 559
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Search completed: March 16, 2006, 17:25:15

Job time : 23 secs







Db 1201 ATCTACTTCAACTCCTTCTCTGGAATCCTTCCAGGGCTTCTTTGTGTGTGTCTACTGT 1260  
QY 1261 TTCTCTCAATAGTGGTCCGTTCTGCCATCCGGAAGAGTGGCACCGGTGGCAGGCAAG 1320  
Db 1261 TTCTCTCAATAGTGGTCCGTTCTGCCATCCGGAAGAGTGGCACCGGTGGCAGGCAAG 1320  
QY 1321 CACTCGATCCGTCGCGAGTGGCCGCGTGCATGTCATCCCACTCCCAACCCCGTGC 1380  
Db 1321 CACTCGATCCGTCGCGAGTGGCCGCGTGCATGTCATCCCACTCCCAACCCCGTGC 1380  
QY 1381 AGCTTTACAGCATCAAGCATCCAGCATCCAGCATCCAGCATCCAGCATCCAGCATCC 1440  
Db 1381 AGCTTTACAGCATCAAGCATCCAGCATCCAGCATCCAGCATCCAGCATCCAGCATCC 1440  
QY 1441 CAAAGAGCTGTGCTGGGGGATGAGCGCCAGGCTCCCTGACCACTGCTGTGGAGT 1500  
Db 1441 CAAAGAGCTGTGCTGGGGGATGAGCGCCAGGCTCCCTGACCACTGCTGTGGAGT 1500  
QY 1501 GACCTGTTAGGTCTCATGCCCCACTCCCCCAGGAGCAGTGGCACTGACAGCCTGGGGGG 1560  
Db 1501 GACCTGTTAGGTCTCATGCCCCACTCCCCCAGGAGCAGTGGCACTGACAGCCTGGGGGG 1560  
QY 1561 CGCCTCTCCCTGCGAGCGTG 1582  
Db 1561 CGCCTCTCCCTGCGAGCGTG 1582

## RESULT 3

ABX11840

ID ABX11840 standard; cDNA; 1582 BP.

XX

AC ABX11840;

XX

DT 07-MAY-2003 (first entry)

XX

DE Human cDNA encoding hCRF-RAI, splice variant.

XX

KW Human; as; gene; corticotropin releasing factor receptor; hCRF-RAI;  
KW Cushing's disease; pituitary tumour; Alzheimer's disease;  
KW melancholic depression; anorexia nervosa; chronic stress; alcoholism;  
KW hypercortisolemia; gastrointestinal disorder; irritable bowel syndrome;  
KW pre-eclampsia; pregnancy-induced complication; arthritis; abortion;  
twinning.

XX

OS Homo sapiens.

XX

PH Key Location/Qualifiers

FT CDS 82..1416

FT /\*tag= a

FT /product= "hCRF-RAI splice variant"

XX

US6482608-B1.

XX

PD 19-NOV-2002.

XX

XX 26-MAY-2000; 2000US-00580734.

XX

XX 18-JUN-1993; 93US-00079320.

PR 23-AUG-1993; 93US-00110286.

PR 25-MAY-1994; 94WO-US005908.

PR 09-DEC-1994; 94US-00353537.

PR 17-JAN-1995; 95US-00374009.

PR 07-JUN-1995; 95US-00483139.

PR 12-NOV-1998; 98US-00191724.

XX

(SALK ) SALK INST BIOLOGICAL STUDIES.

XX

XX Perrin MH, Chen R, Lewis KA, Vale WM, Donaldson CJ, Sawchenko P;

XX WPI; 2003-287359/28.

DR P-PDB; ABG76402.

XX

PT Novel cell line expressing nucleic acid expression vector comprising

QY 481 CTCCTGGTGGCCCTTTGTCTCTTTCTGCGGCTCAGGCCAGGCTGCACCCATTTGGGGTGAC 540  
DB 481 CTCCTGGTGGCCCTTTGTCTCTTTCTGCGGCTCAGGCCAGGCTGCACCCATTTGGGGTGAC 540  
QY 541 CAGGCAGATGGAGCCCTTGAGGTGGGGCTTCATGAGTGGTCCCATTTCAAGGTTGGA 600  
DB 541 CAGGCAGATGGAGCCCTTGAGGTGGGGCTTCATGAGTGGTCCCATTTCAAGGTTGGA 600  
QY 601 AGGAGCATCCGGTGCCTCGGAACATCATCCTGGAACCTCATCTCGGCTTCATCCTG 660  
DB 601 AGGAGCATCCGGTGCCTCGGAACATCATCCTGGAACCTCATCTCGGCTTCATCCTG 660  
QY 661 CGCAAGCCACCTGGTTCGTGCTCCAGCTTAACATGAGCCCGAGTCCACGAGCAAC 720  
DB 661 CGCAAGCCACCTGGTTCGTGCTCCAGCTTAACATGAGCCCGAGTCCACGAGCAAC 720  
QY 721 GTGGGCTGGTGAGGTGGTGACAGCGCTCAACAATCTTCCATGTGACCAACTCTTTC 780  
DB 721 GTGGGCTGGTGAGGTGGTGACAGCGCTCAACAATCTTCCATGTGACCAACTCTTTC 780  
QY 781 TGGATGTTGGCGAGGGCTGTACTACCTGCACACAGCCATCGTCTCACTACTCCACTGAC 840  
DB 781 TGGATGTTGGCGAGGGCTGTACTACCTGCACACAGCCATCGTCTCACTACTCCACTGAC 840  
QY 841 CGGCTGGCAAAATGGATGTTTCATCTGCAATTGGCTGGGGTGTGCCCTTCCCATCATTTGTG 900  
DB 841 CGGCTGGCAAAATGGATGTTTCATCTGCAATTGGCTGGGGTGTGCCCTTCCCATCATTTGTG 900  
QY 901 GCCTGGGCCAATGGGAGGCTGTACTACGACAATGAGAAGTCTGTTTGGCAAAAGGCT 960  
DB 901 GCCTGGGCCAATGGGAGGCTGTACTACGACAATGAGAAGTCTGTTTGGCAAAAGGCT 960  
QY 961 GGGGTGTACACCGACTACATCTACCGAGGCCCATGATCTCGTCTCTGTGATCAATTTTC 1020  
DB 961 GGGGTGTACACCGACTACATCTACCGAGGCCCATGATCTCGTCTCTGTGATCAATTTTC 1020  
QY 1021 ATCTTCTTTTCAACATGTCGCGATCTCTCATGACCAAGTCTCGGGGATCCACACGCTCT 1080  
DB 1021 ATCTTCTTTTCAACATGTCGCGATCTCTCATGACCAAGTCTCGGGGATCCACACGCTCT 1080  
QY 1081 GAGACCAATTCAGTACAGGAGGCTGTGAAAGCCATCTGCTGCTGCTGCGCCCTCTGGGC 1140  
DB 1081 GAGACCAATTCAGTACAGGAGGCTGTGAAAGCCATCTGCTGCTGCTGCGCCCTCTGGGC 1140  
QY 1141 ATCACTTACATGCTGTTCTTTCGTCATATCCCGGGAGGATGAGGTCTCCCGGTCGTTCTTC 1200  
DB 1141 ATCACTTACATGCTGTTCTTTCGTCATATCCCGGGAGGATGAGGTCTCCCGGTCGTTCTTC 1200  
QY 1201 ATCTACTTCAACTCTTCTCGTGGAACTCTTCCAGGGCTTCTTGTGTCTGTGTTCTACTGT 1260  
DB 1201 ATCTACTTCAACTCTTCTCGTGGAACTCTTCCAGGGCTTCTTGTGTCTGTGTTCTACTGT 1260  
QY 1261 TTCTCTCAATAGTGGTCCGTTCTGCCATCCGAGAGGTTGGCACCGGTGGCAGGACAAG 1320  
DB 1261 TTCTCTCAATAGTGGTCCGTTCTGCCATCCGAGAGGTTGGCACCGGTGGCAGGACAAG 1320  
QY 1321 CACTTCGATCCGTCGCGAGTGGCCGTCGTCATATCCCACTCCCAACCCCGTGC 1380  
DB 1321 CACTTCGATCCGTCGCGAGTGGCCGTCGTCATATCCCACTCCCAACCCCGTGC 1380  
QY 1381 AGCTTTTCAAGCATCAAGCAGTCCACAGCAGTCTGAGCTGGCAGGTCATGGAGCAGCCC 1440  
DB 1381 AGCTTTTCAAGCATCAAGCAGTCCACAGCAGTCTGAGCTGGCAGGTCATGGAGCAGCCC 1440  
QY 1441 CAAAGAGCTGTGGTGGGGGATGACGGCAGGCTCCCTGACCACTTGTGAGGT 1500  
DB 1441 CAAAGAGCTGTGGTGGGGGATGACGGCAGGCTCCCTGACCACTTGTGAGGT 1500  
QY 1501 GACCTGTTAGTCTCATGCGCCACTTCCCGCAGGAGCAGCTGACAGCTGGGGGGG 1560  
DB 1501 GACCTGTTAGTCTCATGCGCCACTTCCCGCAGGAGCAGCTGACAGCTGGGGGGG 1560

QY 1561 CCGCTCTCCCTGCGAGCCGTG 1582  
DB 1561 CCGCTCTCCCTGCGAGCCGTG 1582  
RESULT 4  
ADJ65809  
ID ADJ65809 standard; cDNA; 1582 BP.  
XX AC ADJ65809;  
XX DT 20-MAY-2004 (first entry)  
XX DE Human corticotropin-releasing factor receptor CRF-RA2 cDNA.  
XX KW Human; corticotropin-releasing factor receptor; CRF-RA2; ss; gene;  
KW Alzheimer's disease; melancholic depression; anorexia nervosa;  
KW Cushing's disease; hypercortisolemia; alcoholism;  
KW gastrointestinal disorder; irritable bowel syndrome; inflammation;  
KW Addison's disease; cardiac perfusion; blood pressure; hypotension.  
XX OS Homo sapiens.  
XX FH Key Location/Qualifiers  
FT CDS 82..1416  
FT /\*tag= a /product= "CRF-RA2"  
XX PN US2004039173-A1.  
XX PD 26-FEB-2004.  
XX PF 26-AUG-2003; 2003US-00649193.  
XX PR 18-JUN-1993; 93US-00079320.  
XX PR 23-AUG-1993; 93US-00110286.  
XX PR 25-MAY-1994; 94WO-US005908.  
XX PR 09-DEC-1994; 94US-0035537.  
XX PR 07-JUN-1995; 95US-0048139.  
XX PR 12-NOV-1998; 98US-00191724.  
XX (SALK ) SALK INST BIOLOGICAL STUDIES.  
XX PI Perrin MH, Chen R, Lewis KA, Vale WW, Donaldson CJ, Sawchenko P;  
XX WPI; 2004-203293/19.  
XX P-PSDB; ADJ65810.  
XX PT New mammalian G protein-coupled corticotropin-releasing factor receptor  
XX protein, useful in diagnosing and treating Alzheimer's disease, anorexia  
XX nervosa, Cushing's disease, alcoholism, irritable bowel syndrome or  
XX hypotension.  
XX PS Claim 1; SEQ ID NO 14; 44pp; English.  
XX CC The invention relates to an isolated mammalian G protein-coupled  
XX corticotropin-releasing factor (CRF) receptor protein or polypeptide from  
XX Rat, Mouse or human appearing as ADJ65801, ADJ65803, ADJ65805, or  
XX ADJ65810, encoded by the nucleic acids appearing as ADJ65800, ADJ65802,  
XX ADJ65804, or ADJ65809. Also included are a composition comprising CRF-R,  
XX an antibody generated against CRF-R and a diagnostic kit, for assaying  
XX for the presence in biological fluids of CRF-R protein, protein analogues  
XX and/or fragments, comprising CRF-R) and/or one or more antibodies. The  
XX protein, polynucleotide or composition is useful in diagnosing and  
XX treating Alzheimer's disease, melancholic depression, anorexia nervosa,  
XX Cushing's disease, hypercortisolemia or alcoholism, gastrointestinal  
XX disorders (e.g. irritable bowel syndrome) or physiological conditions  
XX (e.g. inflammation or Addison's disease), in regulating cardiac perfusion  
XX and in modulating blood pressure, thus combat hypotension. The present  
XX sequence encodes human splice variant CRF-RA2.  
SQ Sequence 1582 BP; 286 A; 518 C; 437 G; 341 T; 0 U; 0 Other;

Query Match	100.0%	Score 1582	DB 12	Length 1582
Best Local Similarity	100.0%	Prod. No. 0		
Matches 1582	Conservative	0	Mismatches	0
Qy	1	CGAGCCCGCAGCCGCGCCCGTTCCTCTGGGATGTCCGTAGGACCGGGCATTCAGGAC	60	
Db	1	CGAGCCCGCAGCCGCGCCCGTTCCTCTGGGATGTCCGTAGGACCGGGCATTCAGGAC	60	
Qy	61	GGTAGCCGAGCGAGCCCGGAGGATGGAGGGCACCCGCAAGCTCCGTCGTCGAAGGCCCTT	120	
Db	61	GGTAGCCGAGCGAGCCCGGAGGATGGAGGGCACCCGCAAGCTCCGTCGTCGAAGGCCCTT	120	
Qy	121	CTCCTTCTGGGCGTGAACCCCGTCTCTGCTCTCCCTCAGACACAGCACTGCGAGGCGTG	180	
Db	121	CTCCTTCTGGGCGTGAACCCCGTCTCTGCTCTCCCTCAGACACAGCACTGCGAGGCGTG	180	
Qy	181	TCCCTGGCCAGCAACATCTCAGGACTCAGTGCAACGATCCGCTGGACCTCATTTGGCACC	240	
Db	181	TCCCTGGCCAGCAACATCTCAGGACTCAGTGCAACGATCCGCTGGACCTCATTTGGCACC	240	
Qy	241	TGCTGGCCCCGCGAGCCCTGCGGGCGAGCTAGTGCTTCGGGCCCTGCCCTCTTTTTCAT	300	
Db	241	TGCTGGCCCCGCGAGCCCTGCGGGCGAGCTAGTGCTTCGGGGCCTGCCCTCTTTTTCAT	300	
Qy	301	GGTGTCGCTACAATAACAACAAATGGCTACCGGAGTGCTTGGCCAAATGGCAGCTGG	360	
Db	301	GGTGTCGCTACAATAACAACAAATGGCTACCGGAGTGCTTGGCCAAATGGCAGCTGG	360	
Qy	361	GCGCCCGCGTGAAATTAATCTCGAGTGCCAGGAGATCTCAATGAGGAGAAAAAGCAAG	420	
Db	361	GCGCCCGCGTGAAATTAATCTCGAGTGCCAGGAGATCTCAATGAGGAGAAAAAGCAAG	420	
Qy	421	GTGCATACCAATGTGCGAGTCATCACTCAACTCGGCCCACTGTATCTCCCTGGTGCC	480	
Db	421	GTGCATACCAATGTGCGAGTCATCACTCAACTCGGCCCACTGTATCTCCCTGGTGCC	480	
Qy	481	CTCTGTGTGCTTTGTCTCTTTCTCGGCTCAGGCCAGGCTGCACCCCAATGGGGTGAC	540	
Db	481	CTCTGTGTGCTTTGTCTCTTTCTCGGCTCAGGCCAGGCTGCACCCCAATGGGGTGAC	540	
Qy	541	CAGCAGATGGAGCCCTGGAGGTGGGGCTCCATGGAAGTGGTGGCCCAATTCAGGTTGCA	600	
Db	541	CAGCAGATGGAGCCCTGGAGGTGGGGCTCCATGGAAGTGGTGGCCCAATTCAGGTTGCA	600	
Qy	601	AGGAGCATCCGGTGCCTCGGAAAACATCATCCACTGGAACTCATCTCGGCTTCATCCTG	660	
Db	601	AGGAGCATCCGGTGCCTCGGAAAACATCATCCACTGGAACTCATCTCGGCTTCATCCTG	660	
Qy	661	CGCAACGCCACCTGGTTCTGTTCCAGCTAACCAATGAGCCCGAGGTCCACAGAGCAAC	720	
Db	661	CGCAACGCCACCTGGTTCTGTTCCAGCTAACCAATGAGCCCGAGGTCCACAGAGCAAC	720	
Qy	721	GTGGGCTGGTGAGGTTGGTGACAGCCGCTCAAACTACTTCATGTCGAACAACTTCTTC	780	
Db	721	GTGGGCTGGTGACAGTTGGTGACAGCCGCTCAAACTACTTCATGTCGAACAACTTCTTC	780	
Qy	781	TGGATGTTTGGCGAGGCGTGCTACTCTGCACACAGCCATCGTGCTCACTACTCCACTGAC	840	
Db	781	TGGATGTTTGGCGAGGCGTGCTACTCTGCACACAGCCATCGTGCTCACTACTCCACTGAC	840	
Qy	841	CGGCTGCGCAATGGATGTTTCATCTGATTTGGCTGGGGTGTGGCCCTTCCCCATCTGTG	900	
Db	841	CGGCTGCGCAATGGATGTTTCATCTGATTTGGCTGGGGTGTGGCCCTTCCCCATCTGTG	900	
Qy	901	GCCTGGGCCCATTGGGAAGCTGTACTACGAAATGAGAAGTGTCTGGTTTGGCAAGGCGCT	960	
Db	901	GCCTGGGCCCATTGGGAAGCTGTACTACGAAATGAGAAGTGTCTGGTTTGGCAAGGCGCT	960	
Qy	961	GGGCTGTACACCGACTACATCTACAGGGCCCCATGATCTCTGGTCTGCTGATCAATTTTC	1020	
Db	961	GGGCTGTACACCGACTACATCTACAGGGCCCCATGATCTCTGGTCTGCTGATCAATTTTC	1020	
Qy	1021	ATCTTCTCTTTTCAACATCGTCCGATCCTCATGACCAAGCTCCGGGATCCACCAAGCTCT	1080	

[illegible]



XX WPI: 1995-052077/07.  
DR P-PSDB; AAR69519.  
XX  
PT Isolated corticotropin releasing factor receptor and nucleic acid - also  
PT antibodies, useful for diagnosis and treatment of Cushing's disease,  
PT pituitary tumours etc., also to identify specific agonists and  
PT antagonists.  
XX  
PS Claim 6; Page 63; 84pp; English.  
XX  
CC The protein encoded by this sequence can be used to determine CRF (e.g.  
CC over- or under-production, high levels of CRF late in pregnancy may  
CC indicate risk of premature labor). Cells expressing the protein are used  
CC to identify e.g. antibodies, which can be used to modulate signal  
CC transduction activity mediated by CRF receptors. Typical applications are  
CC in the treatment of Cushing's disease, pituitary tumors, etc. (Updated on  
CC 25-MAR-2003 to correct PN field.)  
XX  
SQ Sequence 1495 BP; 271 A; 496 C; 403 G; 325 T; 0 U; 0 Other;

Query Match 88.4%; Score 1398; DB 2; Length 1495;  
Best Local Similarity 94.5%; Pred. No. 0;  
Matches 1495; Conservative 0; Mismatches 0; Indels 87; Gaps 1;

QY 1 CGAGCCCGAGCCGCGCGGTTCTCTGGGATGTCCTAGGACCCGGGCAATTCAGGAC 60  
DB 1 CGAGCCCGAGCCGCGCGGTTCTCTGGGATGTCCTAGGACCCGGGCAATTCAGGAC 60

QY 61 GGTAGCCGAGCGAGCCGAGGATGGGAGGACCCGCGAGTCCGTCTCGTCAAGGCCCTT 120  
DB 61 GGTAGCCGAGCGAGCCGAGGATGGGAGGACCCGCGAGTCCGTCTCGTCAAGGCCCTT 120

QY 121 CTCCTCTCGGGGTGAACCCCGTCTCTGCTCCCTCCAGGACCACTGCGAGAGCTG 180  
DB 121 CTCCTCTCGGGGTGAACCCCGTCTCTGCTCCCTCCAGGACCACTGCGAGAGCTG 180

QY 181 TCCTGCGCCAGCAACATCTCAGGACTCGAGTGCAGCAATGGCTCCGTCGTCATTTGCTAT 240  
DB 181 TCCTGCGCCAGCAACATCTCAGGACTCGAGTGCAGCAATGGCTCCGTCGTCATTTGCTAT 240

QY 241 TGTGCGCCCGAGCCCTGCGGGGACGTAGTGGTTCGGGCGCTGCGCCCTGCTTTTCTAT 300  
DB 241 TGTGCGCCCGAGCCCTGCGGGGACGTAGTGGTTCGGGCGCTGCGCCCTGCTTTTCTAT 300

QY 301 GGTGTCGCTACAAATACCAAAACAATGGCTACCGGGAGTGCCTGGCAATGGCAGCTGG 360  
DB 301 GGTGTCGCTACAAATACCAAAACAATGGCTACCGGGAGTGCCTGGCAATGGCAGCTGG 360

QY 361 GCGCCCGCGGTGAATTAATCTCGAGTGCAGAGATCTCAATGAGGAGAAAAAAGCAAG 420  
DB 361 GCGCCCGCGGTGAATTAATCTCGAGTGCAGAGATCTCAATGAGGAGAAAAAAGCAAG 420

QY 421 GTGCACTACCAATGTCGAGTCAATCACTACTGCGGCACTGTATCTCCCTGGTGCC 480  
DB 421 GTGCACTACCAATGTCGAGTCAATCACTACTGCGGCACTGTATCTCCCTGGTGCC 480

QY 481 CTCTGGTGGCTTTGCTCTTTCTGCGGTCAAGGCCAGGCTGCACCCATTTGGGGTGAC 540  
DB 481 CTCTGGTGGCTTTGCTCTTTCTGCGGCTC----- 513

QY 541 CAGGCAAGTGGAGCCCTGGAGGTGGGGGCTCCATGGAGTGGTCCCATTTTCAGTTTGA 600  
DB 514 ----- 513

QY 601 AGGAGCATCGGTGCTCGGAAACATCATCTGAGTGAACCTCATCTCGGCTTCATCTG 660  
DB 514 AGGAGCATCGGTGCTCGGAAACATCATCTGAGTGAACCTCATCTCGGCTTCATCTG 573

QY 661 CGCAAGCCCACTGGTTCTGTTGCTCCAGTAAACATGAGCCCGAGGTCCACAGAGCAAC 720  
DB 574 CGCAAGCCCACTGGTTCTGTTGCTCCAGTAAACATGAGCCCGAGGTCCACAGAGCAAC 633

QY 721 GTGGGCTGGTGAGGTTGGTGACAGCGGCTCAAACTACTTCCATGTGACCAACTTCTTC 780  
DB 634 GTGGGCTGGTGAGGTTGGTGACAGCGGCTCAAACTACTTCCATGTGACCAACTTCTTC 693

QY 781 TGGATGTTGGCGAGGGCTGCTACTACCTGCAACAGCCATCGTGTCTCACTACTCCACTGAC 840  
DB 694 TGGATGTTGGCGAGGGCTGCTACTACCTGCAACAGCCATCGTGTCTCACTACTCCACTGAC 753

QY 841 CGGCTGGCAAAATGGATGTTTCATCTGATTTGGCTGGGGTGTGCCCTTCCCATCATTTGTG 900  
DB 754 CGGCTGGCAAAATGGATGTTTCATCTGATTTGGCTGGGGTGTGCCCTTCCCATCATTTGTG 813

QY 901 GCCTGGGCCAATTCGGAGCTGTACTACGACAATGAGAAGTGTGGTTTGGCAAAAGCCCT 960  
DB 814 GCCTGGGCCAATTCGGAGCTGTACTACGACAATGAGAAGTGTGGTTTGGCAAAAGCCCT 873

QY 961 GGGGTGTACACCGACTACATCTACCGAGGGCCCATGATCTCTGTCTGTGATCAATTC 1020  
DB 874 GGGGTGTACACCGACTACATCTACCGAGGGCCCATGATCTCTGTCTGTGATCAATTC 933

QY 1021 ATCTTCTTTTCAACATCGTCCGATCTCATGACCAAGCTCCGGGATCCACACGCTCT 1080  
DB 934 ATCTTCTTTTCAACATCGTCCGATCTCATGACCAAGCTCCGGGATCCACACGCTCT 993

QY 1081 GAGACCAATTCAGTACAGGAGGCTGTGAAGCCACTCTGTGTGTGCTGCTGCCCTCTCGGC 1140  
DB 994 GAGACCAATTCAGTACAGGAGGCTGTGAAGCCACTCTGTGTGTGCTGCTGCCCTCTCGGC 1053

QY 1141 ATCACTTACATGCTGTTCTTCTGTCATCCCGGGAGGATGAGGTCTCCCGGCTGCTTC 1200  
DB 1054 ATCACTTACATGCTGTTCTTCTGTCATCCCGGGAGGATGAGGTCTCCCGGCTGCTTC 1113

QY 1201 ATCTACTTCAACTCTCTCTGGAATCTTCCAGGGCTCTTTGTGTGTGTGTGTGTGTGT 1260  
DB 1114 ATCTACTTCAACTCTCTCTGGAATCTTCCAGGGCTCTTTGTGTGTGTGTGTGTGTGT 1173

QY 1261 TTCTCAATAGTACGCTCGTCTGTCATCCGGAAGAGTGGCACCGGTGGCAGGACAAG 1320  
DB 1174 TTCTCAATAGTACGCTCGTCTGTCATCCGGAAGAGTGGCACCGGTGGCAGGACAAG 1233

QY 1321 CACTCGATCCGTCGCGAGTGGCCCGTGCATGTCCATCCCACTCCCAACCCCGTGTG 1380  
DB 1234 CACTCGATCCGTCGCGAGTGGCCCGTGCATGTCCATCCCACTCCCAACCCCGTGTG 1293

QY 1381 AGTTTTCACAGCATCAAGCAGTCCACAGAGTCTGAGCTGGCAGGTGATGGAGCAGCCCC 1440  
DB 1294 AGTTTTCACAGCATCAAGCAGTCCACAGAGTCTGAGCTGGCAGGTGATGGAGCAGCCCC 1353

QY 1441 CAAAGAGCTGTGGCTGGGGGATGACGGCCAGGCTCCCTGACCACTGCTGCTGTGAGGT 1500  
DB 1354 CAAAGAGCTGTGGCTGGGGGATGACGGCCAGGCTCCCTGACCACTGCTGCTGTGAGGT 1413

QY 1501 GACTGTGTTAGTCTCATGCCACTCCCGCAGGAGCAGTGGCACTGACAGCTGGGGGGG 1560  
DB 1414 GACTGTGTTAGTCTCATGCCACTCCCGCAGGAGCAGTGGCACTGACAGCTGGGGGGG 1473

QY 1561 CCGCTCTCCCGCTGACAGCCGTG 1582  
DB 1474 CCGCTCTCCCGCTGACAGCCGTG 1495

RESULT 6  
AAT28968  
ID AAT28968 standard; cDNA; 1495 BP.  
XX  
AC AAT28968;  
XX  
DT 21-AUG-1996 (first entry)  
XX  
DE Human CRF receptor A1 cDNA.  
XX  
KW Corticotropin releasing factor receptor; CRF-R; corticoliberin;  
KW signal transduction; db.

XX OS Homo sapiens.  
 XX FH Key Location/Qualifiers  
 XX CDS 89..1329  
 XX FT /\*tag= a  
 XX PN MO9617934-A2.  
 XX PD 13-JUN-1996.  
 XX PF 06-DEC-1995; 95WO-US015909.  
 XX PR 09-DEC-1994; 94US-00353537.  
 XX PR 17-JAN-1995; 95US-00374009.  
 XX PA (SALK ) SALK INST BIOLOGICAL STUDIES.  
 XX PI Perrin MH, Chen R, Lewis KA, Vale MW, Donaldson CJ, Sawchenko P;  
 XX WPI; 1996-287179/29.  
 XX DR P-PSDB; AAR97290.  
 XX PT Isolated corticotropin-releasing factor receptor (CRF-R) - used to  
 XX develop prods. for modulating signal transduction activity mediated by  
 XX CRF-R.  
 XX P8 Claim 6; Page 75-77; 102pp; English.  
 XX CC A cDNA clone (AAR28968), designated CRF-R1, codes for a new G-protein-  
 CC coupled receptor protein (AAR97290), which has high binding affinity for  
 CC corticotropin releasing factor (CRF). It was isolated from a cDNA library  
 CC prep'd. from human pituitary corticotrope adenoma (Cushing's tumour) by  
 CC screening using an expression cloning approach; a splice variant (see  
 CC AAR28969) was also identified. The cDNA can be used as a probe for  
 CC detecting the presence of CRF receptor-encoding nucleic acids in samples  
 CC or for the identification of additional CRF receptors, or can be used for  
 CC prodn. of recombinant CRF receptor, or in gene therapy to target a vector  
 CC to specific cell types  
 XX SQ Sequence 1495 BP; 271 A; 496 C; 403 G; 325 T; 0 U; 0 Other;  
 Query Match 88.4%; Score 1398; DB 2; Length 1495;  
 Best Local Similarity 94.5%; Pred. No. 0;  
 Matches 1495; Conservative 0; Mismatches 0; Indels 87; Gaps 1;  
 QY 1 CGAGCCCGCAGCCGCGCGTTCCTCTGGGATGTCGATAGGACCGGGCATTCAGGAC 60  
 DB 1 CGAGCCCGCAGCCGCGCGTTCCTCTGGGATGTCGATAGGACCGGGCATTCAGGAC 60  
 QY 61 GGTAGCCGAGCGCGCGGATGGGAGGCGACCCGCGCTCGTCTCGTCAAGGCCCTT 120  
 DB 61 GGTAGCCGAGCGCGCGGATGGGAGGCGACCCGCGCTCGTCTCGTCAAGGCCCTT 120  
 QY 121 CTCCTCTGCGGCTGAACCCCGTCTCTGCTCCCTCCAGGACCGAGCTCGGAGGCGCTG 180  
 DB 121 CTCCTCTGCGGCTGAACCCCGTCTCTGCTCCCTCCAGGACCGAGCTCGGAGGCGCTG 180  
 QY 181 TCCTGCGCAGCAACATCTCAGACTGCACTGCAAGCAACGCTCGTGGACCTCATTTGGCACC 240  
 DB 181 TCCTGCGCAGCAACATCTCAGACTGCACTGCAAGCAACGCTCGTGGACCTCATTTGGCACC 240  
 QY 241 TGCTGCGCGCGAGCCCTGCGGGGAGCTAGTGGTTGCGGCCCTGCGCTTTTCTAT 300  
 DB 241 TGCTGCGCGCGAGCCCTGCGGGGAGCTAGTGGTTGCGGCCCTGCGCTTTTCTAT 300  
 QY 301 GGTGTCCGCTACAAATACCAAAATGGCTACCGGAGTGCTTGGCCAAATGGCAGCTGG 360  
 DB 301 GGTGTCCGCTACAAATACCAAAATGGCTACCGGAGTGCTTGGCCAAATGGCAGCTGG 360  
 QY 361 GCCGCCCGCGTGAATTAATCTCCGAGTGCAGGAGATCTCAATGAGGAGAAAAAGCAAG 420  
 DB 361 GCCGCCCGCGTGAATTAATCTCCGAGTGCAGGAGATCTCAATGAGGAGAAAAAGCAAG 420

QY 421 GTGCACTACATGTGCGAGTCAATCAACTACCTGGGCACTGTATCTCCCTGGTGGCC 480  
 DB 421 GTGCACTACATGTGCGAGTCAATCAACTACCTGGGCACTGTATCTCCCTGGTGGCC 480  
 QY 481 CTCCTGGTGGCCTTTGTCTCTTTTGTGGGCTCAGGCGAGGCTGCACCAATTTGGGGTGAC 540  
 DB 481 CTCCTGGTGGCCTTTGTCTCTTTTCTGGGCTC----- 513  
 QY 541 CAGGAGATGGAGCCCTCGAGGTGGGGGCTCCATGAGGTGGTGGCCCAATTCAGGTTGCA 600  
 DB 514 ----- 513  
 QY 601 AGGAGCATCCGGTGCCTGGAAACATCATCTCACTGAACTCATCTCCGCTTTCCTCTG 660  
 DB 514 AGGAGCATCCGGTGCCTGGAAACATCATCTCACTGAACTCATCTCCGCTTTCCTCTG 573  
 QY 661 CGCAACGCCACCTGGTTCGTGTGCTCAAGCTAAACATGAGCCCGAGGTCCACAGAGCAAC 720  
 DB 574 CGCAACGCCACCTGGTTCGTGTGCTCAAGCTAAACATGAGCCCGAGGTCCACAGAGCAAC 633  
 QY 721 GTGGGCTGTGCAAGTGTGTGACAGCGGCTCAACTACTTCCATGTGACCAACTTCTTC 780  
 DB 634 GTGGGCTGTGCAAGTGTGTGACAGCGGCTCAACTACTTCCATGTGACCAACTTCTTC 693  
 QY 781 TGGATGTTCCGGGAGGGCTGTCTACCTGACACAGCCATCGTGTCTCACCTACTCCACTGAC 840  
 DB 694 TGGATGTTCCGGGAGGGCTGTCTACCTGACACAGCCATCGTGTCTCACCTACTCCACTGAC 753  
 QY 841 CGGCTGCGCAATGGATGTTTCATCTGCAATGGGTGGGTGTGCCCCTTCCCAATCATTTGTG 900  
 DB 754 CGGCTGCGCAATGGATGTTTCATCTGCAATGGGTGGGTGTGCCCCTTCCCAATCATTTGTG 813  
 QY 901 GCCTGGGCCATTGGGAAGCTGTACTAGGACATAGAGAAGTGTGTTTGGCAAAAGGCT 960  
 DB 814 GCCTGGGCCATTGGGAAGCTGTACTAGGACATAGAGAAGTGTGTTTGGCAAAAGGCT 873  
 QY 961 GGGGTGTACACCGACTACATCTACACAGGGCCCATGATCCTGTGTCTGTGATCAATTTTC 1020  
 DB 874 GGGGTGTACACCGACTACATCTACACAGGGCCCATGATCCTGTGTCTGTGATCAATTTTC 933  
 QY 1021 ATCTCTCTTTTCAACATCGTCCGCACTCTCATGACCAAGCTCCGGGCATCCACCAAGTCT 1080  
 DB 934 ATCTCTCTTTTCAACATCGTCCGCACTCTCATGACCAAGCTCCGGGCATCCACCAAGTCT 993  
 QY 1081 GAGACCATTCAGTACAGGAAGGCTGTGAAAGCACTCTGTGTGTGTGCTGCTCCCTCTGGGC 1140  
 DB 994 GAGACCATTCAGTACAGGAAGGCTGTGAAAGCACTCTGTGTGTGTGCTGCTCCCTCTGGGC 1053  
 QY 1141 ATCACCTACATGCTGTTCTTGTCAATCCCGGGGAGATGAGTCTCCCGGGTCTGCTTTC 1200  
 DB 1054 ATCACCTACATGCTGTTCTTGTCAATCCCGGGGAGATGAGTCTCCCGGGTCTGCTTTC 1113  
 QY 1201 ATCTACTTCAACTCTCTTCTGGAATCTTTCAGGGGCTTCTTGTGTGTGTGTCTACTGT 1260  
 DB 1114 ATCTACTTCAACTCTCTTCTGGAATCTTTCAGGGGCTTCTTGTGTGTGTGTCTACTGT 1173  
 QY 1261 TTCCTCAATAGTGAAGTCCGTTCCTGCAATCCGGAAGAGTGGCAACCGGTGGCAGGCAAG 1320  
 DB 1174 TTCCTCAATAGTGAAGTCCGTTCCTGCAATCCGGAAGAGTGGCAACCGGTGGCAGGCAAG 1233  
 QY 1321 CACTCGATCCGTGCCCGAGTGGCGCATGTGCTCCATCCCACTCCCAACCCGCTGTC 1380  
 DB 1234 CACTCGATCCGTGCCCGAGTGGCGCATGTGCTCCATCCCACTCCCAACCCGCTGTC 1293  
 QY 1381 AGCTTTTCAAGCATCAAGCAGTCCACAGAGTCTGAGCTGGCAGGCTCATGGAGAGACCCC 1440  
 DB 1294 AGCTTTTCAAGCATCAAGCAGTCCACAGCAGTCTGAGCTGGCAGGCTCATGGAGAGACCCC 1353  
 QY 1441 CAAAGAGCTGTGGCTGGGGGAGTGAAGCGGCTCCCTGACCAAGCTGCTGTGAGGT 1500  
 DB 1354 CAAAGAGCTGTGGCTGGGGGAGTGAAGCGGCTCCCTGACCAAGCTGCTGTGAGGT 1413

QY 1501 GACCTGTAGGCTCTCATGCCCACTCCCGAGGAGAGCTGGCACTGACAGCCTGGGGGG 1560  
Db 1414 GACCTGTAGGCTCTCATGCCCACTCCCGAGGAGAGCTGGCACTGACAGCCTGGGGGG 1473  
QY 1561 CCGCTCTCCCGCTGCGAGCCGTG 1582  
Db 1474 CCGCTCTCCCGCTGCGAGCCGTG 1495

## RESULT 7

AAD44482  
ID AAD44482 standard; cDNA; 1495 BP.  
XX AAD44482;  
AC AAD44482;  
XX  
DT 13-DEC-2002 (first entry)  
XX  
DE Human CRF-RAL cDNA.  
XX  
KW Human; G protein-coupled corticotropin-releasing factor receptor; CRF;  
KW CRF-R; adrenocorticotrophic hormone; irritable bowel syndrome; therapy;  
KW Cushing's syndrome; pituitary tumour; chronic stress; anorexia nervosa;  
KW receptor; alcoholism; CRF-RAL; gene; ss.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT CDS 82..1329  
FT /\*tag= a  
FT /product= "hCRF-RAL protein"  
XX  
PN US200205617-A1.

XX  
PD 09-MAY-2002. 98US-00191724.  
XX  
PF 12-NOV-1998;  
XX  
PR 18-JUN-1993; 93US-00079320.  
PR 23-AUG-1993; 93US-00110286.  
PR 25-MAY-1994; 94WO-US005908.  
PR 09-DEC-1994; 94US-00353537.  
PR 07-JUN-1995; 95US-00483139.  
XX  
PA (PERR/) PERRIN M H.  
PA (CHEN/) CHEN R.  
PA (LEWIS/) LEWIS K A.  
PA (VALE/) VALE W W.  
PA (DONA/) DONALDSON C J.  
PA (SAWC/) SAWCHENKO P.

XX  
PI Perrin MH, Chen R, Lewis KA, Vale MW, Donaldson CJ, Sawchenko P;  
XX  
XX WPI: 2002-462916/49.  
XX P-PSDB; AAE26679.

XX  
PT New isolated recombinant mammalian G protein-coupled corticotropin-  
PT releasing factor receptor protein for treating e.g. Cushing's syndrome,  
PT pituitary tumors, stress, anorexia, alcoholism or irritable bowel  
PT syndrome.

XX  
PS Claim 1; Page 20-22; 44pp; English.

XX  
CC The invention relates to recombinant mammalian G protein-coupled  
CC corticotropin-releasing factor (CRF) receptor (CRF-R) proteins having  
CC high affinity for CRF and nucleic acid molecules encoding such receptor  
CC proteins. Polypeptides of the invention can be used to reduce high levels  
CC of adrenocorticotrophic hormone caused by excess CRF and so can be used  
CC to treat diseases such as Cushing's syndrome, pituitary tumours, chronic  
CC stress, anorexia nervosa, alcoholism and irritable bowel syndrome. They  
CC are used in pharmaceuticals and in the production of antibodies. The  
CC present sequence is human CRF-RAL cDNA

XX  
XX Sequence 1495 BP; 271 A; 496 C; 403 G; 325 T; 0 U; 0 Other;

Query Match 88.4%; Score 1398; DB 6; Length 1495;  
Best Local Similarity 94.5%; Pred. No. 0;  
Matches 1495; Conservative 0; Mismatches 0; Indels 87; Gaps 1;  
QY 1 CGAGCCCGCAGCGCCGCGGTTCTCTGGGATGTCCTAGGACCCGGGCAATTCAGGAC 60  
Db 1 CGAGCCCGCAGCGCCGCGGTTCTCTGGGATGTCCTAGGACCCGGGCAATTCAGGAC 60  
QY 61 GGTAGCCGAGCGAGCCCGGAGGATGGAGGGCAACCCGAGCTCCGTCTCGTCAAGGCCCTT 120  
Db 61 GGTAGCCGAGCGAGCCCGGAGGATGGAGGGCAACCCGAGCTCCGTCTCGTCAAGGCCCTT 120  
QY 121 CTCCTTCTGGGCTGAACCCCGTCTCTGCTCCCTCCAGGACCCGAGCTCCGAGGCTG 180  
Db 121 CTCCTTCTGGGCTGAACCCCGTCTCTGCTCCCTCCAGGACCCGAGCTCCGAGGCTG 180  
QY 181 TCCCTGGCCAGCAACATCTCAGGACTGCAGTGCAGCAACGCGCATCCGTGACCTCATTTGGCACC 240  
Db 181 TCCCTGGCCAGCAACATCTCAGGACTGCAGTGCAGCAACGCGCATCCGTGACCTCATTTGGCACC 240  
QY 241 TGTGTCCTCCGAGCCCTCGGGGAGCTAGTGGTTCGGCCCTGCGCTCTGCTTTTCTAT 300  
Db 241 TGTGTCCTCCGAGCCCTCGGGGAGCTAGTGGTTCGGCCCTGCGCTCTGCTTTTCTAT 300  
QY 301 GGTGTCCTGCTACATATACCAACAAATGCTACCGGGAGTGCCTGGCCATGTCAGCTGG 360  
Db 301 GGTGTCCTGCTACATATACCAACAAATGCTACCGGGAGTGCCTGGCCATGTCAGCTGG 360  
QY 361 GCGCCCGCGTGAAATTTACTCCGAGTCCGAGTCCGAGGAGTCTCAATGAGGAGAAAAAGCAAG 420  
Db 361 GCGCCCGCGTGAAATTTACTCCGAGTCCGAGGAGTCTCAATGAGGAGAAAAAGCAAG 420  
QY 421 GTGCACTACCATGTGCGAGTCAATCAACTACTTGGGCCACTGTATCTCCCTGGTGCC 480  
Db 421 GTGCACTACCATGTGCGAGTCAATCAACTACTTGGGCCACTGTATCTCCCTGGTGCC 480  
QY 481 CTCCTGGTGCCCTTTGTCTCTTTCTGGGCTCAGGCCAGGCTGACCCCATTCGGGTGAC 540  
Db 481 CTCCTGGTGCCCTTTGTCTCTTTCTGGGCTC----- 513  
QY 541 CAGGCAGATGGAGCCCTCGAGGTGGGGCTCCATGAGTGGTGCCCATTTTCAGGTTCGA 600  
Db 514 ----- 513  
QY 601 AGGAGCATCCGGTGCCTGGGAAACATCATCTCACTGGAACCTCATCTCCGCTTTCATCTG 660  
Db 514 AGGAGCATCCGGTGCCTGGGAAACATCATCTCACTGGAACCTCATCTCCGCTTTCATCTG 573  
QY 661 CGCAACGCCACCTGGTTCTGGTCCAGCTAACCATGAGCCCCGAGGTCCACAGAGCAAC 720  
Db 574 CGCAACGCCACCTGGTTCTGGTCCAGCTAACCATGAGCCCCGAGGTCCACAGAGCAAC 633  
QY 721 GTGGGCTGTGCAAGTTGTGACAGCCGGCTCAACTTCTTCCATGTGACCAACTTCTTC 780  
Db 634 GTGGGCTGTGCAAGTTGTGACAGCCGGCTCAACTTCTTCCATGTGACCAACTTCTTC 693  
QY 781 TGGATGTTCCGGGAGGGCTGTACTCTGCACACAGCCATCGTGTCTCAGCTACTCCACTGAC 840  
Db 694 TGGATGTTCCGGGAGGGCTGTACTCTGCACACAGCCATCGTGTCTCAGCTACTCCACTGAC 753  
QY 841 CGGCTCGCAATGAGATTTCACTGCAATTTGGCTGGGGTGTGCCCTTCCCATCATTTGTG 900  
Db 754 CGGCTCGCAATGAGATTTCACTGCAATTTGGCTGGGGTGTGCCCTTCCCATCATTTGTG 813  
QY 901 GCTTGGGCCATTTGGGAGGCTGTACTAGCAATGAGAGTGTGTTTGGCAAGAGCCCT 960  
Db 814 GCTTGGGCCATTTGGGAGGCTGTACTAGCAATGAGAGTGTGTTTGGCAAGAGCCCT 873  
QY 961 GGGGTGTACACCGACTACATCTACAGGGGCCCATGATCTCTGCTCTGCTGATCAATTC 1020  
Db 874 GGGGTGTACACCGACTACATCTACAGGGGCCCATGATCTCTGCTCTGCTGATCAATTC 933



QY 481 CTCTGGTGGCTTTGTCTCTTCTGCGGCTCAGGCCAGGCTGCACCCATTGGGGTGAC 540  
Db 481 CTCTGGTGGCTTTGTCTCTTCTGCGGCTC----- 513  
QY 541 CAGGCAGATGGAGCCTTGGAGTGGGGCTCCATGGAGTGGTCCCATTTTCAGGTTGGA 600  
Db 514 ----- 513  
QY 601 AGAGAGATCCGGTGCCTGCGAATCATCATCTGGAACCTCATCTCGGCTTTCATCTG 660  
Db 514 AGAGAGATCCGGTGCCTGCGAATCATCATCTGGAACCTCATCTCGGCTTTCATCTG 573  
QY 661 CGCAAGCCGACCTGGTTCGTGGTCCAGTAAACATGAGCCCGAGGTCCACACAGAGCAAC 720  
Db 574 CGCAAGCCGACCTGGTTCGTGGTCCAGTAAACATGAGCCCGAGGTCCACACAGAGCAAC 633  
QY 721 GTGGGCTGGTGACAGGTTGGTGACAGCGCGCTCAACACTTACTTCCATGTGACCAACTTCTTC 780  
Db 634 GTGGGCTGGTGACAGGTTGGTGACAGCGCGCTCAACACTTACTTCCATGTGACCAACTTCTTC 693  
QY 781 TGGATGTTGGCGAGGCTGTCTACTGCAACAGCCATCGTGTCTCACTACTCCACTGAC 840  
Db 694 TGGATGTTGGCGAGGCTGTCTACTGCAACAGCCATCGTGTCTCACTACTCCACTGAC 753  
QY 841 CGGCTGGCAATGGATGTTTCATCTGCAATGGCTGGGCTGTCCTCCCATCATTTGTG 900  
Db 754 CGGCTGGCAATGGATGTTTCATCTGCAATGGCTGGGCTGTCCTCCCATCATTTGTG 813  
QY 901 GCCTGGGCCATTTGGAGCTGTACTAGCAATGAGAGTGTGGTTTGGCAAAAGGCGCT 960  
Db 814 GCCTGGGCCATTTGGAGCTGTACTAGCAATGAGAGTGTGGTTTGGCAAAAGGCGCT 873  
QY 961 GGGGTTGTACACCGACTACATCTACCGAGGCCCCATGATCTCTGTCTGTGATCAATTTTC 1020  
Db 874 GGGGTTGTACACCGACTACATCTACCGAGGCCCCATGATCTCTGTCTGTGATCAATTTTC 933  
QY 1021 ATCTTCTTTTCAACATCGTCCGATCTCTATGACCAAGTCTCGGGGATCCACCAAGTCT 1080  
Db 934 ATCTTCTTTTCAACATCGTCCGATCTCTATGACCAAGTCTCGGGGATCCACCAAGTCT 993  
QY 1081 GAGACATTCAGTACAGGAGGCTGTGAAGCCACTCTGTGTCTGTGCTGCCCTCTCTGGGC 1140  
Db 994 GAGACATTCAGTACAGGAGGCTGTGAAGCCACTCTGTGTCTGTGCTGCCCTCTCTGGGC 1053  
QY 1141 ATCACTTACATGCTGTTCTTCTGTCATTCCTGGGAGGATGAGTCTCTCCGGGTCGTCTTC 1200  
Db 1054 ATCACTTACATGCTGTTCTTCTGTCATTCCTGGGAGGATGAGTCTCTCCGGGTCGTCTTC 1113  
QY 1201 ATCTACTTCACTCTCTCTGGAATCTCTCCAGGCTTCTTTGTGTGTGTCTACTGT 1260  
Db 1114 ATCTACTTCACTCTCTCTGGAATCTCTCCAGGCTTCTTTGTGTGTGTCTACTGT 1173  
QY 1261 TTCTCTCAATAGTGGTCCGTTCTGCCATCCGGAAGAGTGGCACCGGTGGCAGGACAAG 1320  
Db 1174 TTCTCTCAATAGTGGTCCGTTCTGCCATCCGGAAGAGTGGCACCGGTGGCAGGACAAG 1233  
QY 1321 CACTTCGATCCGTCGCGAGTGGCCGTCGTCATCTCCCACTCCCAACCCCGTGC 1380  
Db 1234 CACTTCGATCCGTCGCGAGTGGCCGTCGTCATCTCCCACTCCCAACCCCGTGC 1293  
QY 1381 AGCTTTTCAAGCATCAAGAGTGCACAGAGTCTGAGCTGGAGGTCAATGGAGAGCCCC 1440  
Db 1294 AGCTTTTCAAGCATCAAGAGTGCACAGAGTCTGAGCTGGAGGTCAATGGAGAGCCCC 1353  
QY 1441 CAAAGAGTGTGGTGGGGGATGACGGCCAGGCTCCCTGACCACTGCTGTGGAGT 1500  
Db 1354 CAAAGAGTGTGGTGGGGGATGACGGCCAGGCTCCCTGACCACTGCTGTGGAGT 1413  
QY 1501 GACTGTGTAGTGTCTCATGCCCCACTTCCCGCCAGGAGCAGTGGCACTGACAGCTTGGGGGG 1560  
Db 1414 GACTGTGTAGTGTCTCATGCCCCACTTCCCGCCAGGAGCAGTGGCACTGACAGCTTGGGGGG 1473  
QY 1561 CGGCTCTCCCGCTTCAGCCGCTG 1582

Db 1474 CGGCTCTCCCGCTTCAGCCGCTG 1495  
RESULT 9  
ABX11833  
ID ABX11833 standard; cDNA; 1495 BP.  
XX  
AC ABX11833;  
XX  
DT 07-MAY-2003 (first entry)  
XX Human cDNA encoding corticotropin releasing factor receptor, hCRF-RAL.  
XX Human; ss; gene; corticotropin releasing factor receptor; hCRF-RAL;  
KW Cushing's disease; pituitary tumour; Alzheimer's disease;  
KW melancholic depression; anorexia nervosa; chronic stress; alcoholism;  
KW hypercortisolemia; gastrointestinal disorder; irritable bowel syndrome;  
KW pre-eclampsia; pregnancy-induced complication; arthritis; abortion;  
KW twinning.  
XX Homo sapiens.  
XX  
XX Key Location/Qualifiers  
CDS 82..1329  
FT /\*tag= a  
FT /product= "hCRF-RAL"  
XX US6482608-B1.  
XX  
XX 19-NOV-2002.  
XX  
XX 26-MAY-2000; 2000US-00580734.  
XX  
XX 18-JUN-1993; 93US-00079320.  
PR 23-AUG-1993; 93US-00110286.  
PR 25-MAY-1994; 94WO-US005908.  
PR 09-DEC-1994; 94US-00353537.  
PR 17-JAN-1995; 95US-00374009.  
PR 12-JUN-1995; 95US-00483139.  
PR 12-NOV-1998; 98US-00191724.  
XX  
XX (SALK ) SALK INST BIOLOGICAL STUDIES.  
XX Perrin MH, Chen R, Lewis KA, Vale WW, Donaldson CJ, Sawchenko P;  
XX WPI; 2003-287359/28.  
XX P-PSDB; ABG76046.  
XX Novel cell line expressing nucleic acid expression vector comprising  
PT nucleic acid encoding human corticotropin releasing factor (CRF) receptor  
PT useful for reducing high adrenocorticotropin hormone, by binding to CRF.  
XX  
XX Example 1; Col 37-40; 42pp; English.  
XX The invention relates to a cell line expressing a recombinant  
CC corticotropin releasing factor receptor (CRF-R) encoded by a nucleic acid  
CC expression vector, or a cell line containing a nucleic acid vector  
CC encoding a recombinant CRF-R. The vector encodes human CRF-R, subtype A,  
CC variant 1 (hCRF-RAL). Also included is expressing a recombinant CRF  
CC receptor in a suitable host cell, by expressing the vector, where the  
CC nucleic acid encodes CRF-R that binds CRF or nucleic acid degenerate to  
CC the naturally occurring nucleic acid. The cell line is useful for  
CC expressing hCRF-RAL protein by recombinant techniques and in binding  
CC assays using CRF-R which are used for rapidly screening large number of  
CC compounds to determine which compounds are capable of binding to CRF-R,  
CC and for identifying new CRF-like ligands. The polypeptides expressed by  
CC the cell line inhibit CRF binding to CRF-R and can inhibit CRF-induced  
CC adrenocorticotropin hormone (ACTH) release in vitro by several cells, and  
CC so are useful for reducing high ACTH levels caused by excess CRF, and for  
CC treating Cushing's disease, pituitary tumours, Alzheimer's disease, and  
CC melancholic depression, anorexia nervosa, chronic stress, alcoholism and  
CC hypercortisolemia. The proteins are also useful for treating



FH Key Location/Qualifiers  
 FT CDS 82..1329  
 FT /\*tag= a  
 FT /product= "CFR-RA1"  
 XX  
 XX US2004039173-A1.  
 XX  
 XX 26-FEB-2004.  
 XX  
 XX 26-AUG-2003; 2003US-00649193.  
 XX  
 XX 18-JUN-1993; 93US-00079320.  
 XX 23-AUG-1993; 93US-00110286.  
 XX 25-MAY-1994; 94WO-US0005908.  
 XX 09-DEC-1994; 94US-00353537.  
 XX 07-JUN-1995; 95US-00483139.  
 XX 12-NOV-1998; 98US-00191724.  
 XX  
 XX (SALK ) SALK INST BIOLOGICAL STUDIES.  
 XX  
 XX Ferrin MH, Chen R, Lewis KA, Vale WW, Donaldson CJ, Sawchenko P;  
 XX WPI; 2004-203293/19.  
 XX P-PSDB; ADJ65797.  
 XX  
 XX New mammalian G protein-coupled corticotropin-releasing factor receptor  
 PT protein, useful in diagnosing and treating Alzheimer's disease, anorexia  
 PT nervosa, Cushing's disease, alcoholism, irritable bowel syndrome or  
 PT hypotension.  
 XX  
 XX Example 1; SEQ ID NO 1; 44pp; English.  
 XX  
 CC The invention relates to an isolated mammalian G protein-coupled  
 CC corticotropin-releasing factor (CRF) receptor protein or polypeptide from  
 CC Rat, Mouse or human appearing as ADJ65801, ADJ65803, ADJ65805, or  
 CC ADJ65810, encoded by the nucleic acids appearing as ADJ65800, ADJ65802,  
 CC ADJ65804, or ADJ65809. Also included are a composition comprising CRF-R,  
 CC an antibody generated against CRF-R and a diagnostic kit, for assaying  
 CC for the presence in biological fluids of CRF-R protein, protein analogues  
 CC and/or fragments, comprising CRF-R) and/or one or more antibodies. The  
 CC protein, polynucleotide or composition is useful in diagnosing and  
 CC treating Alzheimer's disease, melancholic depression, anorexia nervosa,  
 CC Cushing's disease, hypercortisolemia or alcoholism, gastrointestinal  
 CC disorders (e.g. irritable bowel syndrome) or physiological conditions  
 CC (e.g. inflammation or Addison's disease), in regulating cardiac perfusion  
 CC and in modulating blood pressure, thus combat hypotension. The present  
 CC sequence encodes human CRF-RA1.  
 XX  
 XX Sequence 1495 BP; 271 A; 496 C; 403 G; 325 T; 0 U; 0 Other;  
 XX  
 XX Query Match 88.4%; Score 1398; DB 12; Length 1495;  
 XX Best Local Similarity 94.5%; Pred. No. 0;  
 XX Matches 1495; Conservative 0; Mismatches 0; Indels 87; Gaps 1;  
 XX  
 QY 1 CGAGCCGCGAGCCGCGCGGTTCTCTGGGATGTCCTAGGACCCGGGCAATTCAGGAC 60  
 DB 1 CGAGCCGCGAGCCGCGCGGTTCTCTGGGATGTCCTAGGACCCGGGCAATTCAGGAC 60  
 QY 61 GGTAGCCGAGCGAGCCGCGGATGGGAGGCGCCCGCAGCTCCGTCCTCGTCAAGGCCCTT 120  
 DB 61 GGTAGCCGAGCGAGCCGCGGATGGGAGGCGCCCGCAGCTCCGTCCTCGTCAAGGCCCTT 120  
 QY 121 CTCCTTCTGGGGCTGAACCCCGTCTCTGCTCCCTCCAGGACCCAGCACTCGGAGAGCCTG 180  
 DB 121 CTCCTTCTGGGGCTGAACCCCGTCTCTGCTCCCTCCAGGACCCAGCACTCGGAGAGCCTG 180  
 QY 181 TCCTTGGCCAGCAACATCTCAGGACTGCACTGCAAGCATCCGCTGGAACCTCATTTGGCACC 240  
 DB 181 TCCTTGGCCAGCAACATCTCAGGACTGCACTGCAAGCATCCGCTGGAACCTCATTTGGCACC 240  
 QY 241 TGCTGGCCCGCAGCCCTGCGGGGCGAGCTAGTGGTTGCGGCCCTGCGCTTTTCTAT 300  
 DB 241 TGCTGGCCCGCAGCCCTGCGGGGCGAGCTAGTGGTTGCGGCCCTGCGCTTTTCTAT 300

QY 301 GGTGTCCGCTACAATACCAACAAATAGGCTACCGGAGTGCTTGGCCAAATGCGAGCTGG 360  
 DB 301 GGTGTCCGCTACAATACCAACAAATAGGCTACCGGAGTGCTTGGCCAAATGCGAGCTGG 360  
 QY 361 GCGCCCGCGGTGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 420  
 DB 361 GCGCCCGCGGTGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 420  
 QY 421 GTGCACTACCATGTGCGAGTCACTCACTACCTGCGGCCACTGTATCTCCCTGGTGGCC 480  
 DB 421 GTGCACTACCATGTGCGAGTCACTCACTACCTGCGGCCACTGTATCTCCCTGGTGGCC 480  
 QY 481 CTCCTGGTGGCCCTTTGCTCTCTTTCTGGGCTCAGGCGAGGTGCAACCAATTTGGGGTGAC 540  
 DB 481 CTCCTGGTGGCCCTTTGCTCTCTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 513  
 QY 541 CAGGCAGATGGAGCCCTCGGAGGTGGGGGCTCCATGGATGGTGGCCCTTTCAGGTTTCGA 600  
 DB 541 ----- 513  
 QY 601 AGGAGCATCCGCTGCTCGGAAACATCACTCACTGGAACCTCACTCCGCTTTCATCTG 660  
 DB 514 AGGAGCATCCGCTGCTCGGAAACATCACTCACTGGAACCTCACTCCGCTTTCATCTG 573  
 QY 661 CGCAACGCCACCTGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720  
 DB 574 CGCAACGCCACCTGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 633  
 QY 721 GTGGGCTGTGTGAGGTGGTGACAGCGGCTCACTCACTTCTGATGTGACCACTTCTTC 780  
 DB 634 GTGGGCTGTGTGAGGTGGTGACAGCGGCTCACTCACTTCTGATGTGACCACTTCTTC 693  
 QY 781 TGGATGTTGGCGAGGGCTGCTACCTGCAACAGCCATCGTGTCTCACTACTTCCACTGAC 840  
 DB 694 TGGATGTTGGCGAGGGCTGCTACCTGCAACAGCCATCGTGTCTCACTACTTCCACTGAC 753  
 QY 841 CGGCTCGCAAAATGGAATGTTCACTGATGCTGGGTGGGTGGGTGGGTGGGTGGGTGGGTGG 900  
 DB 754 CGGCTCGCAAAATGGAATGTTCACTGATGCTGGGTGGGTGGGTGGGTGGGTGGGTGGGTGG 813  
 QY 901 GCTTGGGCCATTTGGGAGCTGTACTACGCAATGAGAGTGTGTTTGGCAAAAGGSCCT 960  
 DB 814 GCTTGGGCCATTTGGGAGCTGTACTACGCAATGAGAGTGTGTTTGGCAAAAGGSCCT 873  
 QY 961 GGGGTGTACACCGACTACATCTACAGGGGCCCATGATCTGCTGCTGCTGCTGCTGCTGCT 1020  
 DB 874 GGGGTGTACACCGACTACATCTACAGGGGCCCATGATCTGCTGCTGCTGCTGCTGCTGCT 933  
 QY 1021 ATCTTCTTTTCAACATGCTCGCATCTCATGACCAAGCTCCGGGCAATCCACACGCTCT 1080  
 DB 934 ATCTTCTTTTCAACATGCTCGCATCTCATGACCAAGCTCCGGGCAATCCACACGCTCT 993  
 QY 1081 GAGACCATTCAGTACAGGAGGCTGTGAAGCCACTCTGCTGCTGCTGCTGCTGCTGCTGCTG 1140  
 DB 994 GAGACCATTCAGTACAGGAGGCTGTGAAGCCACTCTGCTGCTGCTGCTGCTGCTGCTGCT 1053  
 QY 1141 ATCACTTACATGCTGTTCTTCTGTCATCCCGGGAGGATGAGGTCTCCCGGGTCTGCTTC 1200  
 DB 1054 ATCACTTACATGCTGTTCTTCTGTCATCCCGGGAGGATGAGGTCTCCCGGGTCTGCTTC 1113  
 QY 1201 ATCTACTTCACTCTCTTCTGGAATCTTTCAGGGCTTCTTTGTTGTTGTTGTTGTTGTTGTT 1260  
 DB 1114 ATCTACTTCACTCTCTTCTGGAATCTTTCAGGGCTTCTTTGTTGTTGTTGTTGTTGTTGTT 1173  
 QY 1261 TTCTCTCAATGAGGTCCGTTCTGTCATCCGGAAGGTTGGCACCGGTGGAGGCAAG 1320  
 DB 1174 TTCTCTCAATGAGGTCCGTTCTGTCATCCGGAAGGTTGGCACCGGTGGAGGCAAG 1233  
 QY 1321 CACTCGATCCGTCGCCGAGTGGCCCGTGCATGTCCATCCCACTCCCACTCCCACTCCCACTCC 1380  
 DB 1234 CACTCGATCCGTCGCCGAGTGGCCCGTGCATGTCCATCCCACTCCCACTCCCACTCCCACTCC 1293



QY 1381 AGCTTTACAGCATCAAGCAGTCCACGACAGTCTGAGCTGGCAGGTCAATGAGCAGCCCC 1440  
Db 1294 AGCTTTACAGCATCAAGCAGTCCACGACAGTCTGAGCTGGCAGGTCAATGAGCAGCCCC 1353  
QY 1441 CAAAGAGCTGTGGCTGGGGGATGAGCGCCAGCGCTCCCTGACACCCCTGCTGTGAGGT 1500  
Db 1354 CAAAGAGCTGTGGCTGGGGGATGAGCGCCAGCGCTCCCTGACACCCCTGCTGTGAGGT 1413  
QY 1501 GACCTGTTAGGTCTCATGCCCCACTCCCCCAGGAGCAGCTGGCACTGACAGCCCTGGGGGG 1560  
Db 1414 GACCTGTTAGGTCTCATGCCCCACTCCCCCAGGAGCAGCTGGCACTGACAGCCCTGGGGGG 1473  
QY 1561 CCGCTCTCCCTCCGACGCGTG 1582  
Db 1474 CCGCTCTCCCTCCGACGCGTG 1495

RESULT 11  
AAS62243/c  
ID AAS62243 standard; cDNA; 2579 BP.  
AC AAS62243,  
XX  
DT 14-FEB-2002 (first entry)  
XX  
XX cDNA sequence #30 encoding novel human secreted protein.  
XX  
XX Human secreted protein; hyperproliferative disorder; autoimmune disorder;  
KW immune deficiency disorder; blood disorder; inflammatory disorder;  
KW infectious disorder; gene therapy; antimicrobial; hepatotropic;  
KW immunosuppressive; antirheumatic; ss.  
XX  
OS Homo sapiens.  
XX  
XX W020017291-A2.  
XX  
XX 18-OCT-2001.  
XX  
XX 29-MAR-2001; 2001WO-US010485.  
XX  
XX 06-APR-2000; 2000US-0195604P.  
PR  
XX (GEMY ) GENETICS INST INC.  
XX  
XX Wong GG, Clark HF, Fachtel K, Agostino MJ, Howes SH, Resnick RJ;  
PI Gulukota K, Graham JR;  
PI  
XX WPI; 2002-010900/01.  
XX  
XX New polynucleotides encoding secreted proteins useful for treating e.g.  
PT asthma, HIV and Crohn's disease.  
PT  
XX  
PS Claim 1; Page 86-87; 391pp; English.  
XX  
XX The present invention relates to the isolation of novel cDNA sequences  
CC which encode human secreted proteins. The cDNA sequences have been  
CC derived from a variety of human tissues. The invention also provides a  
CC method for producing proteins from these polynucleotide sequences. The  
CC proteins are useful for identifying compounds that modulate their  
CC activity and production, and the cell is also useful for identifying  
CC compounds that modulate expression of the polynucleotide sequences  
CC encoding the secreted proteins. The sequences of the invention are useful  
CC for treating diseases such as hyperproliferative disorders (e.g. cancer),  
CC immune deficiency disorders (e.g. severe combined immunodeficiency  
CC (SCID)), autoimmune disorders (e.g. multiple sclerosis), blood disorders  
CC (e.g. thrombocytopenia), inflammatory disorders (e.g. arthritis) and  
CC infectious disorders (e.g. hepatitis). The polynucleotide sequences of  
CC the invention are also useful in gene therapy. AAS62214-AAS62838  
CC represent the cDNA sequences of the invention that encode for novel human  
CC secreted proteins

Sequence 2579 BP; 501 A; 733 C; 840 G; 505 T; 0 U; 0 Other;

Query Match 88.4%; Score 1398; DB 6; Length 2579;  
Best Local Similarity 94.5%; Pred. No. 0;  
Matches 1495; Conservative 0; Mismatches 0; Indels 87; Gaps 1;  
QY 1 CGAGCCCGCAGCGCGCGCGTTCCTCTGGGATGTCCGTAGGACCCCGGGCAATTCAGGAC 60  
Db 2420 CGAGCCCGCAGCGCGCGCGTTCCTCTGGGATGTCCGTAGGACCCCGGGCAATTCAGGAC 2361  
QY 61 GGTAGCCGAGCCAGCGCGCGGAGGATGGAGGGCACCCGCGAGCTCCGTCTCGTCAAGGCCCTT 120  
Db 2360 GGTAGCCGAGCCAGCGCGCGGAGGATGGAGGGCACCCGCGAGCTCCGTCTCGTCAAGGCCCTT 2301  
QY 121 CTCCTTCTGGGCTGAACCCCGCTCTCTGCTCCCTCCAGGACCAAGCACTGCGAGAGCCCTG 180  
Db 2300 CTCCTTCTGGGCTGAACCCCGCTCTCTGCTCCCTCCAGGACCAAGCACTGCGAGAGCCCTG 2241  
QY 181 TCCCTGGCCAGCAACATCTCAGGACTGCACTGCAACAGCATCCGTGGAACCTCATTTGGCACC 240  
Db 2240 TCCCTGGCCAGCAACATCTCAGGACTGCACTGCAACAGCATCCGTGGAACCTCATTTGGCACC 2181  
QY 241 TGCTGGCCCGCAGCGCGCTGGGGGAGCTAGTGGTTGGGCCCTGCGCTTCTTTCTAT 300  
Db 2180 TGCTGGCCCGCAGCGCGCTGGGGGAGCTAGTGGTTGGGCCCTGCGCTTCTTTCTAT 2121  
QY 301 GGTGTCCGCTACATACACAAATGGCTACCGGGAGTGGCTTGGCCAAATGGCAGCTGG 360  
Db 2120 GGTGTCCGCTACATACACAAATGGCTACCGGGAGTGGCTTGGCCAAATGGCAGCTGG 2061  
QY 361 GCGCCCGCGGTGAATTACTCCGAGTGGCAGGAGATCTCAATGAGAGAGAAAAAGCAAG 420  
Db 2060 GCGCCCGCGGTGAATTACTCCGAGTGGCAGGAGATCTCAATGAGAGAGAAAAAGCAAG 2001  
QY 421 GTGCACTACCATGTGCGAGTCACTCAACTACTCTGGGCCACTGTATCTCCCTGGTGGCC 480  
Db 2000 GTGCACTACCATGTGCGAGTCACTCAACTACTCTGGGCCACTGTATCTCCCTGGTGGCC 1941  
QY 481 CTCCTGGTGGCCCTTTGTCTCTTTTGTGGCGCTCAGGCCAGGCTGCACCCCAATTTGGGTGAC 540  
Db 1940 CTCCTGGTGGCCCTTTGTCTCTTTTGTGGCGCTC----- 1908  
QY 541 CAGGCAGATGGAGCCCTGGAGGTGGGGGCTCCATAGAGTGGTGGCCCAATTCAGGTTCGA 600  
Db 1907 ----- 1908  
QY 601 AGGAGCATCCGGTGGCTGGGAACATCATCTCACTGGAACTCATCTCGGCCCTTCATCTCCG 660  
Db 1907 AGGAGCATCCGGTGGCTGGGAACATCATCTCACTGGAACTCATCTCGGCCCTTCATCTCCG 1848  
QY 661 CGCAACGCCACCTGGTTTCGTGGTCCAGCTAACCATGAGCCCGAGGTCCACAGAGCAAC 720  
Db 1847 CGCAACGCCACCTGGTTTCGTGGTCCAGCTAACCATGAGCCCGAGGTCCACAGAGCAAC 1788  
QY 721 GTGGGCTGTGAGGTGTGTGACAGCGGCTTAACTACTTCAATGTGACCAACTTCTTTC 780  
Db 1787 GTGGGCTGTGAGGTGTGTGACAGCGGCTTAACTACTTCAATGTGACCAACTTCTTTC 1728  
QY 781 TGGATGTTCCGGGAGGCGTCTACCTGACACAGCCATCGTCTCACCTTCCACTGAC 840  
Db 1727 TGGATGTTCCGGGAGGCGTCTACCTGACACAGCCATCGTCTCACCTTCCACTGAC 1668  
QY 841 CGGCTCGCAAAATGGAATGTTCACTGTGCAATGGGTGGGTGTGCCCTTCCCCCATCATTTG 900  
Db 1667 CGGCTCGCAAAATGGAATGTTCACTGTGCAATGGGTGGGTGTGCCCTTCCCCCATCATTTG 1608  
QY 901 GCTTGGGCCAATTTGGGAAGCTGTACTACGACAAATGAGAAAGTGTGTTTGGCAAAAGCCCT 960  
Db 1607 GCTTGGGCCAATTTGGGAAGCTGTACTACGACAAATGAGAAAGTGTGTTTGGCAAAAGCCCT 1548  
QY 961 GGGGTGTACACCGACTACATCTACAGGGGCCCAATGATCTCGTCTCTGATCAATTTTC 1020  
Db 1547 GGGGTGTACACCGACTACATCTACAGGGGCCCAATGATCTCGTCTCTGATCAATTTTC 1488  
QY 1021 ATCTTCTTTTCAACATCGTCGCGCATCTCATGACCAAGCTCGGGGCATCCACCACTCT 1080



```
Db 1487 ATCTTCTTTTCAACATGTCGCGCATCTCTATGACCAAGTCCGGGCATCCACAGTCT 1428
Qy 1081 GAGACCAATTCAGTACAGGAGGCTGTGAAGCCACATCTGTGTCTGTCTGCCCTCTCTGGGC 1140
Db 1427 GAGACCAATTCAGTACAGGAGGCTGTGAAGCCACATCTGTGTCTGTCTGCCCTCTCTGGGC 1368
Qy 1141 ATCACTACATGCTGTCTCTCTCAATCCCGGGAGGATGAGTCTCCGGGTCTCTTC 1200
Db 1367 ATCACTACATGCTGTCTCTCTCAATCCCGGGAGGATGAGTCTCTCCGGGTCTCTTC 1308
Qy 1201 ATCTACTTCAACTCTCTCTGGAATCTTCCAGGGCTTCTTGTGTCTGTCTACTGT 1260
Db 1307 ATCTACTTCAACTCTCTCTGGAATCTTCCAGGGCTTCTTGTGTCTGTCTACTGT 1248
Qy 1261 TTCTCTCAATAGTGAAGTCCGTCTTGCATCCGGAAGAGTGGCACCGGTGGCAGGACAAG 1320
Db 1247 TTCTCTCAATAGTGAAGTCCGTCTTGCATCCGGAAGAGTGGCACCGGTGGCAGGACAAG 1188
Qy 1321 CACTCATCTGTCGCGAGTGGCCGTCGATGTCATGCCATCTCCCACTCCCAACCCGTGTC 1380
Db 1187 CACTCATCTGTCGCGAGTGGCCGTCGATGTCATGCCATCTCCCACTCCCAACCCGTGTC 1128
Qy 1381 AGCTTTTCAAGCATCAAGCAGTCCACAGCAGTCTGAGTGGCAGGTCAATGGACGCCCC 1440
Db 1127 AGCTTTTCAAGCATCAAGCAGTCCACAGCAGTCTGAGTGGCAGGTCAATGGACGCCCC 1068
Qy 1441 CAAAGAGCTGTGCTGGGGGATGACGGCCAGCGTCTCTGACCACTCTGCTGTGAGGT 1500
Db 1067 CAAAGAGCTGTGCTGGGGGATGACGGCCAGCGTCTCTGACCACTCTGCTGTGAGGT 1008
Qy 1501 GACCTGTAGTCTCATGCCCCTATCCGCCAGGAGCAGTGGGCTGACAGCTTGGGGGG 1560
Db 1007 GACCTGTAGTCTCATGCCCCTATCCGCCAGGAGCAGTGGGCTGACAGCTTGGGGGG 948
Qy 1561 CGGCTCTCCCGTCGACCGTG 1582
Db 947 CGGCTCTCCCGTCGACCGTG 926

RESULT 12
AD029851
ID AD029851 standard; cDNA; 2536 BP.
XX
AC AD029851;
XX
XX AD029851;
XX
DT 29-JUL-2004 (first entry)
XX
DE Human GPCR CRHR1 polynucleotide, SEQ ID NO:953.
XX
KW G protein-coupled receptor; GPCR; drug screening; diagnosis;
KW transgenic mouse; neurological disorder; adrenal gland disorder;
KW colon disorder; intestinal disorder; cardiovascular disorder;
KW muscular disorder; blood disorder; immune disorder; bone disorder;
KW joint disorder; metabolic disorder; nutritive disorder; cancer;
KW kidney disorder; liver disorder; lung disorder; breast disorder;
KW ovary disorder; uterus disorder; prostate disorder; testis disorder;
KW skin disorder; stomach disorder; pancreas disorder; spleen disorder;
KW thymus disorder; thyroid disorder; antiparkinsonian; antianemic;
KW cytostatic; antiinflammatory; vasotropic; antiangiinal; antiarrhythmic;
KW CNS; central nervous system; respiratory; antidiarrhoeic; antidiabetic;
KW viricide; hepatotropic; antibacterial; antianemic; antiseborrhoeic;
KW dermatological; antitumor; antithyroid; antiallergic; anorectic;
KW immunosuppressive; nephrotropic; gene therapy; GPCR modulator; human;
KW gene; ss.
XX
OS Homo sapiens.
XX
XX WO2004040000-A2.
XX
XX 13-MAY-2004.
XX
PF 09-SEP-2003; 2003WO-US028226.
```

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XX
PR 09-SEP-2002; 2002US-0409303P.
PR 09-APR-2003; 2003US-0461329P.
XX
XX (PRIM-) PRIMAL INC.
XX
PI Gaitanaris GA, Bergmann JE, Gragerov A, Hohmann J, Li P;
PI Madisen L, McIlwain KL, Pavlova MN, Vassiliadis D, Zeng H;
XX
XX WPI; 2004-390329/36.
XX
XX P-PSDB; ADO29265.
XX
XX Novel mammalian G protein coupled receptors, useful for identifying
XX compounds that modulates diagnosing and treating disease condition
XX associated with GPCR dysfunction e.g. autoimmune disease, angina
XX pectoris, Parkinson's disease.
XX
XX Claim 151; SEQ ID NO 953; 542pp; English.
XX
XX The invention relates to human and mouse G protein-coupled receptors
XX (GPCRs) and nucleic acids encoding them. The invention also relates to
XX sequences at least 90% identical to the GPCR proteins and nucleic acids
XX of the invention; methods of treating, preventing or diagnosing diseases
XX associated with GPCRs of the invention; methods of screening for
XX compounds useful in the treatment of GPCR-related diseases; a transgenic
XX mouse comprising a GPCR gene of the invention; a mouse comprising a
XX mutation in a GPCR transgene or in an endogenous GPCR gene; cells derived
XX from the transgenic mice; kits comprising several mice, each of which has
XX a mutation in a different GPCR gene of the invention; and kits comprising
XX probes which hybridise to GPCR polynucleotides of the invention. The
XX invention further discloses variants of the GPCR polypeptides and vectors
XX comprising a GPCR nucleic acid. The GPCR nucleic acids and proteins may
XX be used in the diagnosis, treatment or prevention of a wide variety of
XX diseases including neurological disorders (e.g., Alzheimer's disease,
XX depression, diabetic neuropathy, Parkinson's disease or schizophrenia);
XX disorders of the adrenal gland; disorders of the colon or intestine
XX (e.g., Crohn's disease, diarrhoea, food poisoning or irritable bowel
XX syndrome); cardiovascular disorders (e.g., angina, cardiac arrhythmia or
XX myocardial infarction); muscular disorders; blood disorders (e.g.,
XX anaemia or leukaemia); immune disorders (e.g., autoimmune disorders or
XX AIDS); bone and joint disorders (e.g., osteoarthritis, rheumatoid
XX arthritis, gout or osteoporosis); metabolic or nutritive disorders (e.g.,
XX obesity, enzyme deficiency-related diseases or vitamin deficiency-related
XX diseases); and disorders of the kidney, liver, breast, ovary,
XX uterus, prostate, testis, skin, stomach, pancreas, spleen, thymus and
XX thyroid (e.g., cancers). The present sequence represents a GPCR-encoding
XX nucleic acid of the invention. Note: The full sequence data for this
XX patent did not form part of the printed specification; those sequences
XX not shown were obtained in electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 2536 BP; 478 A; 836 C; 724 G; 498 T; 0 U; 0 Other;
XX
Qy Query Match 88.3%; Score 1396.4; DB 12; Length 2536;
Qy Best Local Similarity 94.4%; Pred. No. 0;
Qy Matches 1494; Conservative 0; Mismatches 1; Indels 87; Gaps 1;
Qy
Db 1 CGAGCCCGCAGCGCCGCGGTCCTCTGGGATGTCCTAGGACCGCGGCATTTCAGGAC 60
Db 146 CGAGCCCGCAGCGCCGCGGTCCTCTGGGATGTCCTAGGACCGCGGCATTTCAGGAC 205
Qy 61 GGTAGCCGAGCGAGCCGAGGATGGAGGCGACCCCGAGCTCCGTCGTCGTCGAGGCCCTT 120
Db 206 GGTAGCCGAGCGAGCCGAGGATGGAGGCGACCCCGAGCTCCGTCGTCGTCGAGGCCCTT 265
Qy 121 CTCCTTCTGGGCTGAACCCCGTCTCTGCTCCCTCCAGGACCGAGCACTGGAGGCGCTG 180
Db 266 CTCCTTCTGGGCTGAACCCCGTCTCTGCTCCCTCCAGGACCGAGCACTGGAGGCGCTG 325
Qy 181 TCCCTGGCCAGCAACATCTCAGGACTGCGAGTCAAGCGCAAGCTCCGTCATTGGCACC 240
Db 326 TCCTGGCCAGCAACATCTCAGGACTGCGAGTCAAGCGCAAGCTCCGTCATTGGCACC 385
```

QY 241 TGCTGGCCCGCAGCCCTGCGGGGCAAGTAGTGGTTGCGCCCTGCGCTGCTTTTCTAT 300  
DB TGCTGGCCCGCAGCCCTGCGGGGCAAGTAGTGGTTGCGCCCTGCGCTGCTTTTCTAT 445  
QY 301 GGTGTCCGCTACAAATACCAAAATGGCTACCGGGAGTGCCTTGGCAATGGCAGCTGG 360  
DB GGTGTCCGCTACAAATACCAAAATGGCTACCGGGAGTGCCTTGGCAATGGCAGCTGG 505  
QY 361 GCCGCCCGCTGAATTAATCCGAGTGCACGAGATCCTCAATGAGGAGAAAAAGCAAG 420  
DB GCCGCCCGCTGAATTAATCCGAGTGCACGAGATCCTCAATGAGGAGAAAAAGCAAG 565  
QY 421 GTGCACTACCAATGTGCGAGTCAATCAATACCTACCTGGGCCACTGTATCTCCCTGGTGGCC 480  
DB GTGCACTACCAATGTGCGAGTCAATCAATACCTACCTGGGCCACTGTATCTCCCTGGTGGCC 625  
QY 481 CTGCTGGTGGCTTTGTCTCTTTCTGCGGCTACGCCAGGCTGCACCCATTTGGGGTGAC 540  
DB CTGCTGGTGGCTTTGTCTCTTTCTGCGGCTC----- 658  
QY 541 CAGGCAGATGGAGCCCTGGAGGTGGGGCTCCATGGAGTGGTGCCTCCCATTTTCAGTTTGA 600  
DB ----- 658  
QY 601 AGGAGCATCGGTGCTCGGAACATCATCCACTGGAACCTCATCTCGCCTTTCATCTG 660  
DB AGGAGCATCGGTGCTCGGAACATCATCCACTGGAACCTCATCTCGCCTTTCATCTG 718  
QY 661 CGCAACGCCACCTGGTTCAGTTCAGCTAAACATGAGCCCGAGGTGCAACGAGCAAC 720  
DB CGCAACGCCACCTGGTTCAGTTCAGCTAAACATGAGCCCGAGGTGCAACGAGCAAC 778  
QY 721 GTGGGCTGGTGCAGTGGTGCAGCGCCTCAACATCTTCCATGTGACCACTCTTTC 780  
DB GTGGGCTGGTGCAGTGGTGCAGCGCCTCAACATCTTCCATGTGACCACTCTTTC 838  
QY 781 TGGATGTTCCGGCAGGGCTGCTACTGTCACACAGCCATCGTGTCTCACTACTCCACTGAC 840  
DB TGGATGTTCCGGCAGGGCTGCTACTGTCACACAGCCATCGTGTCTCACTACTCCACTGAC 898  
QY 841 CGGCTGGCAAAATGGATGTTTCATCTGATTTGGCTGGGGTGTGCCCTTCCCATCATTTGTG 900  
DB CGGCTGGCAAAATGGATGTTTCATCTGATTTGGCTGGGGTGTGCCCTTCCCATCATTTGTG 958  
QY 901 GCCTGGGCCAATGGGAAGCTGTAACGACAATGAGAAGTCTGGTTTGGCAAAAGCCCT 960  
DB GCCTGGGCCAATGGGAAGCTGTAACGACAATGAGAAGTCTGGTTTGGCAAAAGCCCT 1018  
QY 961 GGGGTGTACACCGACTACATCTACCGGGCCCATGATCTCTGCTGCTGTGATCAATTTTC 1020  
DB GGGGTGTACACCGACTACATCTACCGGGCCCATGATCTCTGCTGCTGTGATCAATTTTC 1078  
QY 1021 ATCTTCCTTTTCAACATGTCGCGATCCTCATGACCAAGTCTCGGGGATCCACACAGTCT 1080  
DB ATCTTCCTTTTCAACATGTCGCGATCCTCATGACCAAGTCTCGGGGATCCACACAGTCT 1138  
QY 1081 GAGACCAATTCAGTACAGGAGGTGTAAGGCCACTCTGCTGCTGCTGCTGCTGCTGCTGCTG 1140  
DB GAGACCAATTCAGTACAGGAGGTGTAAGGCCACTCTGCTGCTGCTGCTGCTGCTGCTGCTG 1198  
QY 1141 ATCACTTACATGCTGTTCTTCGTAATTCGCGGAGGATGAGGTCTCCCGGGTCTCTTC 1200  
DB ATCACTTACATGCTGTTCTTCGTAATTCGCGGAGGATGAGGTCTCCCGGGTCTCTTC 1258  
QY 1201 ATCTACTTCAACTCTTCTCGTAATCTTCAGGGCTTCTTGTGTGTGTGTGTGTGTGTGTGT 1260  
DB ATCTACTTCAACTCTTCTCGTAATCTTCAGGGCTTCTTGTGTGTGTGTGTGTGTGTGTGTGT 1318  
QY 1261 TTCTCTCAATAGTGGGTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1320  
DB TTCTCTCAATAGTGGGTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1378  
QY 1321 CACTCGATCCGTGCGGAGTGGGCCGTGCGCATGTCTCCATCCCGCCTCCCAACCCCGTGC 1380

DB 1379 CACTCGATCCGTGCGGAGTGGGCCGTGCGCATGTCTCCCACTCCCAACCCCGTGC 1438  
QY 1381 AGCTTTTCAGCATCAAGCATGTCACAGCATGTCAGCTGGCAGGTTCATGGAGCAGCCCC 1440  
DB 1439 AGCTTTTCAGCATCAAGCATGTCACAGCATGTCAGCTGGCAGGTTCATGGAGCAGCCCC 1498  
QY 1441 CAAAGAGCTGTGCTGCGGGGATGAGCGGCGAGCTCCCTGACCACTGCTGCTGTGAGGT 1500  
DB 1499 CAAAGAGCTGTGCTGCGGGGATGAGCGGCGAGCTCCCTGACCACTGCTGCTGTGAGGT 1558  
QY 1501 GACTCTGTAGTCTCATGCCCCACTCCCCCAGGAGAGCTGGCACTGACAGCTTGGGGGG 1560  
DB 1559 GACTCTGTAGTCTCATGCCCCACTCCCCCAGGAGAGCTGGCACTGACAGCTTGGGGGG 1618  
QY 1561 CGCTCTCCCTTGCAGCCGTG 1582  
DB 1619 CGCTCTCCCTTGCAGCCGTG 1640

RESULT 13  
ADO50782  
ID ADO50782 standard; cDNA; 2536 BP.  
XX  
AC ADO50782;  
XX  
AC ADO50782;  
DT 12-AUG-2004 (first entry)  
XX  
Human corticotropin releasing factor receptor 1, CRFIR, cDNA.  
DE Human; ss; gene; corticotropin releasing factor receptor; CRFIR; CRF2R;  
KW skeletal muscle; muscle atrophy; skeletal muscle dystrophy;  
KW skeletal muscle hypertrophy; surgery; bed rest; broken bone;  
KW infectious disease; AIDS cachexia.  
XX  
Homo sapiens.  
XX  
US2004101911-A1.  
XX  
27-MAY-2004.  
XX  
27-AUG-2003; 2003US-00649852.  
PF  
XX  
06-MAR-2001; 2001US-00799978.  
PR  
XX  
(PROC ) PROCTER & GAMBLE CO.  
PA  
XX  
Isfort RJ, Sheldon RJ;  
PI  
XX  
WPI; 2004-459890/43.  
DR  
XX  
P-PSDB; ADO50783.  
XX  
Identifying compounds for regulating skeletal muscle mass or function, by contacting test compound with vertebrate corticotropin releasing factor2 receptors (CRF2R), selecting compounds that bind or activate CRF2R.  
PS Disclosure; SEQ ID NO 1; 100pp; English.  
XX  
The invention relates to identifying candidate compounds for regulating skeletal muscle mass or function, comprising contacting a test compound with vertebrate corticotropin releasing factor 2 receptors (CRF 2 R), determining if the compound binds to or activates CRF2R, selecting compounds that bind or activate CRF 2 R, and determining if compound increases muscle mass or function in muscle atrophy model. Also included are identifying candidate therapeutic compounds from a group of one or more candidate compounds which have been previously determined to bind to or activate a vertebrate CRF 2 R (comprising administering the candidate compound to a non-human animal and determining whether the candidate compound regulates skeletal muscle mass or function in the treated animal), increasing skeletal muscle mass or function in a subject in which such an increase is desirable (comprising identifying a subject in which an increase in muscle mass or function is desirable and administering to the subject a safe and effective amount of a CRF 2 R



PN US6500938-B1.  
XX 31-DEC-2002.  
XX 30-JAN-1998; 98US-00016434.  
XX 30-JAN-1998; 98US-00016434.  
XX (INCY-) INCYTE GENOMICS INC.  
XX Au-Young J, Seilhamer JJ;  
XX WPI; 2003-352189/33.  
XX  
XX Combination of polynucleotide probes, useful as array elements in a  
XX microarray for monitoring the expression of a number of target  
XX polynucleotides.  
XX  
XX Claim 1; SEQ ID NO 1360; 65pp; English.  
XX  
XX The invention relates to a combination which, comprises a number of  
XX polynucleotide probes comprising a sequence selected from one of the 1490  
XX sequences mentioned in the specification. The combination is useful as an  
XX array element in a microarray for monitoring the expression of a number  
XX of target polynucleotides. The microarray is particularly useful in the  
XX diagnosis and treatment of cancer and immunopathology and neuropathology.  
XX The microarray is useful in diagnostics and treatment regimens, drug  
XX discovery and development, toxicological and carcinogenicity studies,  
XX forensic and pharmacogenomics. The microarray is also useful for  
XX monitoring progression of diseases and for developing sophisticated  
XX profiles for the effects of currently available therapeutic drugs. The  
XX combination is also useful for purifying a subpopulation of mRNAs, cDNAs  
XX and genomic fragments and in research and diagnostic applications. The  
XX array can detect changes in expression in a large number of genes coding  
XX for different signaling pathway populations which can be used to diagnose  
XX various diseases including cancer e.g. adenocarcinoma and leukemia,  
XX immunopathies e.g. AIDS and asthma, neuropathies e.g. Alzheimer's disease  
XX and Parkinson's disease. The present sequence represents a polynucleotide  
XX probe of the invention. Note: The sequence data for this patent did not  
XX form part of the printed specification but was obtained in electronic  
XX seqdata.uspto.gov/sequence.html?DocID=06500938B1  
XX  
XX Sequence 1335 BP; 249 A; 432 G; 350 G; 304 T; 0 U; 0 Other;  
XX  
XX Query Match 84.4%; Score 1335; DB 10; Length 1335;  
XX Best Local Similarity 100.0%; Pred. No. 3.5e-313;  
XX Matches 1335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX  
QY 82 ATGGGAGGGCACCAGCTCCGTCGTCGTCAGGCGCTTCTCTGCGGCTGMAACCCC 141  
DB 1 ATGGGAGGGCACCAGCTCCGTCGTCGTCGTCAGGCGCTTCTCTCTGCGGCTGMAACCCC 60  
QY 142 GTCTCTGCTCTCCCTCCAGGACAGCACTCGAGAGCTGTCCCTGCGCAGCAACATCTCA 201  
DB 61 GTCTCTGCTCTCCCTCCAGGACAGCACTCGAGAGCTGTCCCTGCGCAGCAACATCTCA 120  
QY 202 GGACTGAGTGCAACGCACTCCGTGGAACCTCATTTGGCACTGTGTGGCCCGCAGCCCTGGG 261  
DB 121 GGACTGAGTGCAACGCACTCCGTGGAACCTCATTTGGCACTGTGTGGCCCGCAGCCCTGGG 180  
QY 262 GGGCAGCTAGTGGTTCGGCCCTGCGCTTCTATGTTGTCGCTACATATACCACA 321  
DB 181 GGGCAGCTAGTGGTTCGGCCCTGCGCTTCTATGTTGTCGCTACATATACCACA 240  
QY 322 AACATAGTGTACCGGAGTGCTCGGCAATGGCAGCTGGGCGCCGCGTGAATTACTCC 381  
DB 241 AACATAGTGTACCGGAGTGCTCGGCAATGGCAGCTGGGCGCCGCGTGAATTACTCC 300  
QY 382 GAGTGCAGGAGATCTCAATGAGGAGAAAAAAGCAAGGTGCATACCATGTGCGAGTC 441  
DB 301 GAGTGCAGGAGATCTCAATGAGGAGAAAAAAGCAAGGTGCATACCATGTGCGAGTC 360

QY 442 ATCATCAACTACTCGGCGCACTGTATCTCCCTGTGTGGCCCTCTCTGTGTGCCCTTTGTCTCCTC 501  
DB 361 ATCATCAACTACTCGGCGCACTGTATCTCCCTGTGTGGCCCTCTCTGTGTGCCCTTTGTCTCCTC 420  
QY 502 TTTCTGCGGCTCAGGCGCAGGCTGACCCCATTTGGGFTGACACAGGAGATGGAGCCCTGGAG 561  
DB 421 TTTCTGCGGCTCAGGCGCAGGCTGACCCCATTTGGGFTGACACAGGAGATGGAGCCCTGGAG 480  
QY 562 GTGGGGGCTCCATGGAGTGGTCCCATTTTCAAGTTTCAAGGAGGATCCGCTGCTCCGCA 621  
DB 481 GTGGGGGCTCCATGGAGTGGTCCCATTTTCAAGTTTCAAGGAGGATCCGCTGCTCCGCA 540  
QY 622 AACATCATCACTGGAACCTCATCTCGGCTTTCATCTCGCGCAACGCCACCTGGTTCGTG 681  
DB 541 AACATCATCACTGGAACCTCATCTCGGCTTTCATCTCGCGCAACGCCACCTGGTTCGTG 600  
QY 682 GTCCAGCTAACCATGAGCCCCGAGGFTCCACAGAGCAACGTGGGCTGTGTCAGGTTGGTG 741  
DB 601 GTCCAGCTAACCATGAGCCCCGAGGFTCCACAGAGCAACGTGGGCTGTGTCAGGTTGGTG 660  
QY 742 ACAGCGGCTTACCACTACTTCCATGTGACCAACTTCTTCTGATGTTTCGGCGAGGCTGC 801  
DB 661 ACAGCGGCTTACCACTACTTCCATGTGACCAACTTCTTCTGATGTTTCGGCGAGGCTGC 720  
QY 802 TACCTGCACACAGCCATCGTCTCACCTACTCCACTGACCGGCTGGCAAAATGGATGTTTC 861  
DB 721 TACCTGCACACAGCCATCGTCTCACCTACTCCACTGACCGGCTGGCAAAATGGATGTTTC 780  
QY 862 ATCTGCAATTTGGTGGGTTGTCCTTCCCATCATTTGTGGCTGTGGCCATTTGGGAAGTGTG 921  
DB 781 ATCTGCAATTTGGTGGGTTGTCCTTCCCATCATTTGTGGCTGTGGCCATTTGGGAAGTGTG 840  
QY 922 TACTAGCAAAATGAGGAGTGTGGTTTGGCAAAAGCCCTGGGCTGTACACCGACTACATC 981  
DB 841 TACTAGCAAAATGAGGAGTGTGGTTTGGCAAAAGCCCTGGGCTGTACACCGACTACATC 900  
QY 982 TACCAGGGCCCCATGATGCTGTGCTGTGATCAATTTCTCTCTTTTCAACATCGTC 1041  
DB 901 TACCAGGGCCCCATGATGCTGTGCTGTGATCAATTTCTCTCTTTTCAACATCGTC 960  
QY 1042 CGATCTCTCATGACCAAGCTCCGGGCACTCCACGCTCTGAGACCAATTCAGTACAGGAAG 1101  
DB 961 CGATCTCTCATGACCAAGCTCCGGGCACTCCACGCTCTGAGACCAATTCAGTACAGGAAG 1020  
QY 1102 GCTGTGAAAGCCACTGTGTGCTGCTGCGCCCTCTGGGCACTCACCTACATGCTGTTCTTTC 1161  
DB 1021 GCTGTGAAAGCCACTGTGTGCTGCTGCGCCCTCTGGGCACTCACCTACATGCTGTTCTTC 1080  
QY 1162 GTCAATCCCGGGAGGATGAGGTCCTCCGGGCTGCTTCTCATCTTCAACTCCTTCTCTG 1221  
DB 1081 GTCAATCCCGGGAGGATGAGGTCCTCCGGGCTGCTTCTCATCTTCAACTCCTTCTCTG 1140  
QY 1222 GAATCTCTCCAGGCTTCTTGTGTGTGTCTACTGTTTCTCAATAGTGAAGTCCGT 1281  
DB 1141 GAATCTCTCCAGGCTTCTTGTGTGTGTCTACTGTTTCTCAATAGTGAAGTCCGT 1200  
QY 1282 TCTGCCATCCGGAAGGTTGGCACCGGTGGCAGGACAAAGCACTCGATCCGTCGCCAGTG 1341  
DB 1201 TCTGCCATCCGGAAGGTTGGCACCGGTGGCAGGACAAAGCACTCGATCCGTCGCCAGTG 1260  
QY 1342 GCGCGTGCCATGTCCATCCCACTCCCAACCCGCTGTGAGCTTTTCAAGCATCAAGCAG 1401  
DB 1261 GCGCGTGCCATGTCCATCCCACTCCCAACCCGCTGTGAGCTTTTCAAGCATCAAGCAG 1320  
QY 1402 TCCACAGCAGTCTGA 1416  
DB 1321 TCCACAGCAGTCTGA 1335

RESULT 15  
AD156558  
ID AD156558 standard; DNA; 1335 BP.  
XX

AC ADI56558;  
XX 22-APR-2004 (first entry)  
XX Human polynucleotide probe #1360.  
XX Human; probe; ss; receptor-like polypeptide; transducing polypeptide;  
KW effector-like polypeptide; cancer; immunopathology; neuropathology;  
KW drug development; toxicology; carcinogenicity;  
KW signalling pathway polypeptide; adrenal gland; bladder; bone;  
KW bone marrow; brain; breast; cervix; tumour; immunopathology; AIDS;  
KW diabetes; pancreatitis; osteoporosis; ulcerative colitis; neuropathology;  
KW dementia; amnesia; epilepsy; Alzheimer's disease; depression.  
XX Homo sapiens.  
XX US2004010136-A1.  
XX 15-JAN-2004.  
XX 26-NOV-2002; 2002US-00305720.  
XX 30-JAN-1998; 98US-00016434.  
XX (INCY-) INCYTE GENOMICS INC.  
XX Au-Young J, Seilhamer JJ;  
XX WPI; 2004-090520/09.  
XX New composition comprising polynucleotide probes, useful as array  
PT elements in a microarray for monitoring the expression of target  
PT polynucleotides or purifying a subpopulation of mRNAs, cDNA, or genomic  
PT fragments.  
XX Claim 6; SEQ ID NO 1360; 73pp; English.  
XX The invention relates to a composition of polynucleotide probes  
CC comprising first polynucleotide probes comprising at least a portion of a  
CC gene encoding a receptor-like polypeptide, second polynucleotide probes  
CC comprising at least a portion of a gene encoding a transducing  
CC polypeptide and third polynucleotide probes comprising at least a portion  
CC of a gene encoding an effector-like polypeptide. The probes of the  
CC composition are useful as array elements in a microarray for monitoring  
CC the expression of target polynucleotides. The microarray is useful in the  
CC diagnosis and treatment of cancer, an immunopathology or a  
CC neuropathology. It can also be used for drug discovery and development.  
CC toxicological and carcinogenicity studies, forensics or pharmacogenomics.  
CC Microarrays can also be used for monitoring the progression of diseases  
CC that may be associated with the altered expression of signalling pathway  
CC polypeptides. The composition can also be used to purify a subpopulation  
CC of mRNAs, cDNAs, or genomic fragments in a sample. The expression profile  
CC is also useful for the diagnosis and treatment of cancer, e.g. cancers of  
CC the adrenal gland, bladder, bone, bone marrow, brain, breast or cervix,  
CC an immunopathology, e.g. AIDS, diabetes, pancreatitis, osteoporosis or  
CC ulcerative colitis, or a neuropathology, e.g. dementia, amnesia,  
CC epilepsy, Alzheimer's disease or depression. This sequence represents a  
CC human polynucleotide probe of the invention. Note: The sequence data for  
CC this patent did not form part of the printed specification but was  
CC obtained in electronic format directly from USPTO at  
CC seqdata.uspto.gov/sequence.html.  
XX Sequence 1335 BP; 249 A; 432 C; 350 G; 304 T; 0 U; 0 Other;  
SQ

Query Match 84.4%; Score 1335; DB 12; Length 1335;  
Best Local Similarity 100.0%; Pred. No. 3.5e-313;  
Matches 1335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
82 ATGGAGGGGACCGCAGCTCCGTCCTCGTCAAGGCCCTTCTCTTCCTTGGGGCTGAACCCC 141  
1 ATGGAGGGGACCGCAGCTCCGTCCTCGTCAAGGCCCTTCTCTTCCTTGGGGCTGAACCCC 60  
142 GTCTCTGCTCCCTCCAGGACCGACACTGCGAGAGCGCTGTCCTCGGCCACGACATCTCA 201

Db 61 GTCTCTGCTCCCTCCAGGACCGACACTGGAGAGCGCTGTCCTCGGCCAGCACTCTCA 120  
QY 202 GGACTGCACTGCAACGCATCCGTTGGACCTCATTTGGCACTGTGTCGCCGCCGACCCCTGG 261  
Db 121 GGACTGCACTGCAACGCATCCGTTGGACCTCATTTGGCACTGTGTCGCCGCCGACCCCTGG 180  
QY 262 GGGCAGCTAGTGGTTGGGCCCTGCTGCTTTCTATGTTGTTGCTGCTGCTACATACCA 321  
Db 181 GGGCAGCTAGTGGTTGGGCCCTGCTGCTTTCTATGTTGTTGCTGCTGCTACATACCA 240  
QY 322 AACAAATGGCTACCGGAGTGGCTGGCCCAATGGCAGCTGGGCCGCCGCCGCTGAATTA 381  
Db 241 AACAAATGGCTACCGGAGTGGCTGGCCCAATGGCAGCTGGGCCGCCGCCGCTGAATTA 300  
QY 382 GAGTGGCAGGAGATCCTCAATGAGGAGAAAGCAAGTGCATCAACATGTGCGAGTC 441  
Db 301 GAGTGGCAGGAGATCCTCAATGAGGAGAAAGCAAGTGCATCAACATGTGCGAGTC 360  
QY 442 ATCATCAACTACCTGGGCCACTGTATCTCCCTGGTGGCCCTCTGCTGGCTTGTTCCTC 501  
Db 361 ATCATCAACTACCTGGGCCACTGTATCTCCCTGGTGGCCCTCTGCTGGCTTGTTCCTC 420  
QY 502 TTTCTCGGCTCAGGCCAGGCTGCACCCATTTGGGGTGAC CAGGACAGATGAGGCCCTGGAG 561  
Db 421 TTTCTCGGCTCAGGCCAGGCTGCACCCATTTGGGGTGAC CAGGACAGATGAGGCCCTGGAG 480  
QY 562 GTGGGGCTCCATGGAGTGGTGCCTCCATTTCAAGTTGCAAGGAGCATTCGGTGCCTGCGA 621  
Db 481 GTGGGGCTCCATGGAGTGGTGCCTCCATTTCAAGTTGCAAGGAGCATTCGGTGCCTGCGA 540  
QY 622 AACATCACTACCTGGAACCTCATCTCGGCTTCATCTGCGGCAACGCCACCTGTTGCTG 681  
Db 541 AACATCACTACCTGGAACCTCATCTCGGCTTCATCTGCGGCAACGCCACCTGTTGCTG 600  
QY 682 GTCCAGCTAACCATGAGCCCGGAGTGCAC CAGGACAACTGGGCTGGTGCAGTTGGTG 741  
Db 601 GTCCAGCTAACCATGAGCCCGGAGTGCAC CAGGACAACTGGGCTGGTGCAGTTGGTG 660  
QY 742 ACAGCCGCTTACAACTACTTCCATGTGACCACTTCTCTGATGTTGCGCGAGGGCTGC 801  
Db 661 ACAGCCGCTTACAACTACTTCCATGTGACCACTTCTCTGATGTTGCGCGAGGGCTGC 720  
QY 802 TACTGCA CACAGCCATCTGCTCACTACTCACTGACCGGCTGCGCAAAATGATGTTTC 861  
Db 721 TACTGCA CACAGCCATCTGCTCACTACTCACTGACCGGCTGCGCAAAATGATGTTTC 780  
QY 862 ATCTGCA TTTGGCTGGGGTGGCCCTTCCCATATTTGGCCCTGGGCAATTGGGAAGCTG 921  
Db 781 ATCTGCA TTTGGCTGGGGTGGCCCTTCCCATATTTGGCCCTGGGCAATTGGGAAGCTG 840  
QY 922 TACTACGCAATGAGAAAGTGTGTTTGGCAAAAGGCTGGGGTGTACACCGACTACATC 981  
Db 841 TACTACGCAATGAGAAAGTGTGTTTGGCAAAAGGCTGGGGTGTACACCGACTACATC 900  
QY 982 TACAGGGGCCCCATGATCTGCTGCTGATCAATTTCAATCTCTTTTCAACATCGTC 1041  
Db 901 TACAGGGGCCCCATGATCTGCTGCTGATCAATTTCAATCTCTTTTCAACATCGTC 960  
QY 1042 CGCATCTCATGACCAAGCTCCGGGCACTCCACCACTGAGACCAATTCAGTACAGGAAG 1101  
Db 961 CGCATCTCATGACCAAGCTCCGGGCACTCCACCACTGAGACCAATTCAGTACAGGAAG 1020  
QY 1102 GCTGTGAAGGCCACTCTGCTGCTGCCCTCTCTGGGCATCACTACATGCTGTTCTTC 1161  
Db 1021 GCTGTGAAGGCCACTCTGCTGCTGCCCTCTCTGGGCATCACTACATGCTGTTCTTC 1080  
QY 1162 GTCAATCCCGGGGAGATGAGGTCTCCCGGTCGTCTTCACTACTTCAATCTCTTCCTG 1221  
Db 1081 GTCAATCCCGGGGAGATGAGGTCTCCCGGTCGTCTTCACTACTTCAATCTCTTCCTG 1140  
QY 1222 GAATCTCTCAGGGCTCTTTTGTGTTCTTACTGTTCTTCAATAGTAGAGTCCGT 1281

```

Db 1141 GAATCCTTCCAGGCTTCTTTGTGTGTGTCTTCTACTGTTTCTCAATAGTGAGGTCCGT 1200
Qy 1282 TCTGCCATCCGGAAGAGGTGGCAACCGGTGGCAGGACAAGCACTCGATCCGTGCCCGAGTG 1341
Db 1201 TCTGCCATCCGGAAGAGGTGGCAACCGGTGGCAGGACAAGCACTCGATCCGTGCCCGAGTG 1260
Qy 1342 GCCCGTGCCATGTCCATCCCACTCCCAACCGGTGTCAAGCTTTCAAGCATCAAGCAG 1401
Db 1261 GCCCGTGCCATGTCCATCCCACTCCCAACCGGTGTCAAGCTTTCAAGCATCAAGCAG 1320
Qy 1402 TCCACAGCAGTCTGA 1416
Db 1321 TCCACAGCAGTCTGA 1335

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Search completed: March 17, 2006, 10:52:33  
Job time : 1006 secs

Results 10,11

GenCore version 5.1.7  
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OM nucleic - nucleic search, using sw model

Run on: March 17, 2006, 09:54:53 ; Search time 8122 Seconds  
(without alignments)  
11071.945 Million cell updates/sec

Title: US-10-649-193-14  
Perfect score: 1582  
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Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 1176282

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : GenEmbl.\*

- 1: gb\_ba.\*
- 2: gb\_in.\*
- 3: gb\_env.\*
- 4: gb\_cm.\*
- 5: gb\_ov.\*
- 6: gb\_pat.\*
- 7: gb\_ph.\*
- 8: gb\_pr.\*
- 9: gb\_ro.\*
- 10: gb\_sts.\*
- 11: gb\_sy.\*
- 12: gb\_un.\*
- 13: gb\_vi.\*
- 14: gb\_htg.\*
- 15: gb\_pl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	1582	100.0	1582	6	AR211447 Sequence
2	1582	100.0	1582	6	AR255739 Sequence
3	1582	100.0	1582	6	AR266802 Sequence
4	1582	100.0	1582	6	AR412107 Sequence
5	1398	88.4	1495	6	AR211440 Sequence
6	1398	88.4	1495	6	AR255732 Sequence
7	1398	88.4	1495	6	AR266795 Sequence
8	1398	88.4	1495	6	AR412100 Sequence
9	1396.4	88.3	2536	6	AR442670 Sequence
10	1396.4	88.3	2536	8	HSCRPA
11	1335	84.4	1335	6	AR270797 Sequence
12	1335	84.4	1335	8	HUMCRFRB
13	1283.8	81.2	2374	8	AB078141 Macaca mu
14	1283	81.1	1380	6	I92584 Sequence 1
15	1188	75.1	1285	6	AR442671 Sequence
16	1188	75.1	1285	8	HUMCRFRA
17	1154.2	73.0	10042	6	AX469664 Sequence
18	1151	72.8	1248	6	AX469662 Sequence

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27	1057	66.8	1206	6	AR442673	AR442673 Sequence
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ALIGNMENTS

RESULT 1	AR211447	AR211447	1582 bp	DNA	linear	PAT 20-JUN-2002
LOCUS	Sequence 14 from patent US 6399315.					
DEFINITION	AR211447					
ACCESSION	AR211447.1	GI:21514771				
VERSION	Unknown.					
KEYWORDS	Unknown.					
SOURCE	Unknown.					
ORGANISM	Unclassified.					
REFERENCE	1 (bases 1 to 1582)					
AUTHORS	Perrin,M.H., Chen,R., Lewis,K.A., Vale,W.W. Jr., Donaldson,C.J. and Sawchenko,P.					
TITLE	Screening assays using cloned CRF receptors					
JOURNAL	Patent: US 6399315-A 14 04-JUN-2002;					
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ORIGIN

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Db	61	GCTAGCCGAGCCGAGCCCGCGGATGGAGGCGACCCCGAGCTCCGTCTCGTCAAGGCCCTT	120	
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Db	121	CTCTCTTCTGGGCTGAACCCCGTCTCTGCTCTCCCTCCAGCAGCAGCAGCAGCAGCCTG	180	
Qy	181	TCCTCGGCGAGCAATCTCAGGACTGCAGTGCAGCAAGCATCCCTGGACCTCATTTGGCACC	240	
Db	181	TCCTCGGCGAGCAATCTCAGGACTGCAGTGCAGCAAGCATCCCTGGACCTCATTTGGCACC	240	

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RESULT 2
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DEFINITION Sequence 14 from patent US 6482608.
ACCESSION AR255739
VERSION AR255739.1 GI:27304838
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 1582)
AUTHORS Perrin,M.H., Chen,R., Lewis,K.A., Vale,W.W. Jr., Donaldson,C.J. and Sawchenko,P.
TITLE Cloning and recombinant production of CRF receptor(S)
JOURNAL Patent: US 6482608-A 14 19-NOV-2002;
The Salk Institute for Biological Studies; La Jolla, CA
FEATURES
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ORIGIN
Query Match 100.0%; Score 1582; DB 6; Length 1582;
Best Local Similarity 100.0%; Pred. No. 2.5e-287;
Matches 1582; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 ACCESSION AR412107  
 VERSION AR412107.1 GI:40164666  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 REFERENCE 1 (bases 1 to 1582)  
 AUTHORS Perrin,M.H., Chen,R., Lewis,K.A., Vale,W.W. Jr., Donaldson,C.J. and Sawchenko,P.  
 TITLE Cloning and recombinant production of CFR receptor(s)  
 JOURNAL Patent: US 6638905-A 14 28-OCT-2003;  
 The Salk Institute for Biological Studies; La Jolla, CA  
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Db	814																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																				</
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Qy	841	CGGCTCGCAATGAGATGTTCACTGTGCAATGGCTGGGGTGTGCCCTTCCCCATCATTTG	900	
Db	754	CGGCTCGCAATGAGATGTTCACTGTGCAATGGCTGGGGTGTGCCCTTCCCCATCATTTG	813	
Qy	901	GCTTGGGCCATTTGGGAAGCTGTACTACGACAAATGAGAAGTGTGGTTTGGCAAAAGCCCT	960	
Db	814	GCTTGGGCCATTTGGGAAGCTGTACTACGACAAATGAGAAGTGTGGTTTGGCAAAAGCCCT	873	
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Db	874	GGGGTGTACACCGACTACATCTACAGGGGCCCATCATCTGCTGCTGTGATCAATTTTC	933	
Qy	1021	ATCTTCTTTTCAACATCGTCCGATCTCCATGACCAAGCTCCGGGCATCCACCACTCT	1080	
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RESULT 7  
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LOCUS 1495 bp DNA linear PAT 10-APR-2003  
DEFINITION Sequence 1 from patent US 6495343.  
ACCESSION AR266795  
VERSION AR266795.1 GI:29696119  
KEYWORDS  
SOURCE Unknown.  
ORGANISM  
Unclassified.  
REFERENCE 1 (bases 1 to 1495)  
AUTHORS Ferrin,M.H., Chen,R., Lewis,K.A., Vale,W.W. Jr., Donaldson,C.J. and Sawchenko,P.  
TITLE Cloning and recombinant production of CRF receptor(s)  
JOURNAL Patent: US 6495343-A 1 17-DEC-2002;  
The Salk Institute for Biological Studies; La Jolla, CA  
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LOCUS AR412100 1495 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 1 from patent US 6638905.
ACCESSION AR412100
VERSION AR412100.1 GI:40164659
KEYWORDS
SOURCE Unknown.
ORGANISM
Unclassified.
REFERENCE 1 (bases 1 to 1495)
AUTHORS Perrin,M.H., Chen,R., Lewis,K.A., Vale,W.W. Jr., Donaldson,C.J. and Sawchenko,P.
TITLE Cloning and recombinant production of CFR receptor(s)
JOURNAL Patent: US 6638905-A 1 28-OCT-2003;
The Salk Institute for Biological Studies; La Jolla, CA
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**DEFINITION** Macaca mulatta CRF1 mRNA for corticotropin releasing factor receptor type 1, complete cds.  
**ACCESSION** AB078141  
**VERSION** AB078141.1 GI:38602677  
**KEYWORDS**  
**SOURCE** Macaca mulatta (rhesus monkey)  
**ORGANISM** Macaca mulatta  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Cercopithecoidea; Cercopithecinae; Macaca.  
**REFERENCE**  
**AUTHORS** 1 Oshida, Y., Ikeda, Y., Chaki, S. and Okuyama, S.  
**TITLE** Monkey corticotropin releasing factor1 receptor: cDNA cloning and pharmacological characterization  
**JOURNAL** 2 (bases 1 to 2374)  
**REFERENCE** Direct Submission  
**AUTHORS** Oshida, Y., Ikeda, Y., Chaki, S. and Okuyama, S.  
**TITLE** Submitted (16-JAN-2002) Yuichi Oshida, Medicinal Research Laboratories, Taiho Pharmaceutical Co., Ltd., Medicinal Pharmacology Laboratory; 1-403, Yoshino-cho, Saitama 330-8530, Japan (E-mail: y.oshida@po.rd.taiho.co.jp, Tel: 81-48-669-3028, Fax: 81-48-652-7254)  
**JOURNAL** Location/Qualifiers  
**FEATURES**  
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VERSION  
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SOURCE  
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ORGANISM  
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REFERENCE  
1 (bases 1 to 1248)  
AUTHORS  
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarawal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Perriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.  
TITLE  
Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios  
JOURNAL  
Science 302 (5652), 1960-1963 (2003)



PUBMED 14671302  
REFERENCE 2 (bases 1 to 1248)  
AUTHORS Clark,A.G., Gnanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.  
TITLE Direct Submission  
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA  
COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment.  
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1 (bases 1 to 1248)  
Clark,A.G., Gnanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,  
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,  
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,  
Adams,M.D. and Cargill,M.  
Inferring nonneutral evolution from human-chimp-mouse orthologous  
gene trios  
Science 302 (5652), 1960-1963 (2003)  
JOURNAL  
PUBMED 14671302  
REFERENCE 2 (bases 1 to 1248)  
AUTHORS Clark,A.G., Gnanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.  
TITLE Direct Submission

JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA

COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment.

FEATURES

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LOCUS Mus musculus CRHR1 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.

AY414329

AY414329.1 GI:39770291

GSS.

Mus musculus (house mouse)

ORGANISM

REFERENCE

AUTHORS

Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferreria, S., Wang, G., Zheng, X.H., White, T.J., Shinsky, J.J., Adams, M.D. and Cargill, M.

TITLE

Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios

JOURNAL

Science 302 (5652), 1960-1963 (2003)

PUBLISHED

14671302

REFERENCE

2 (bases 1 to 1248)

AUTHORS

Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferreria, S., Wang, G., Zheng, X.H., White, T.J., Shinsky, J.J., Adams, M.D. and Cargill, M.

TITLE

Direct Submission

JOURNAL

Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA

COMMENT

This sequence was made by sequencing genomic exons and ordering them based on alignment.

FEATURES

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VERSION
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REFERENCE
  1 (bases 1 to 779)
  NIH-MGC http://mgi.nci.nih.gov/.
  National Institutes of Health, Mammalian Gene Collection (MGC)
  Unpublished (1999)
  Contact: Daniela S. Gerhard, Ph.D.
  Office of Cancer Genomics
  National Cancer Institute / NIH
  Bldg. 31 Rm10A07 Bethesda, MD 20892
  Email: cgapbs-x@mail.nih.gov
  Tissue Procurement: GPCR Consortium
  cDNA Library Preparation: GPCR Consortium
  cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LML)
  DNA Sequencing by: Agencourt Bioscience Corporation
  Clone distribution: MGC clone distribution information can be
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ORIGIN

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Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;  
Canis.  
REFERENCE 1 (bases 1 to 581)  
AUTHORS Staten,N.R.  
TITLE Direct Submission (Staten,N.R.)  
JOURNAL Unpublished (2005)  
COMMENT Contact: Nick Staten  
Tel: 636 247 6855  
Email: nicholas.r.staten@pfizer.com.  
FEATURES  
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ORGANISM Pan troglodytes  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Euarchontoglires; Primates; Catarrhini;  
Hominoidea; Pan.  
REFERENCE 1 (bases 1 to 1140)  
AUTHORS Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarawal, A.,  
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,  
Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,  
Adams, M.D. and Cargill, M.  
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous  
gene trios  
JOURNAL Science 302 (5652), 1960-1963 (2003)  
PUBMED 14671302  
REFERENCE 2 (bases 1 to 1140)  
AUTHORS Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarawal, A.,  
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,  
Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,  
Adams, M.D. and Cargill, M.  
TITLE Direct Submission  
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,  
Rockville, MD 20850, USA  
COMMENT This sequence was made by sequencing genomic exons and ordering  
them based on alignment.  
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AUTHORS Ewok-Clover, C.M., Ashwell, C.M., McMurtry, J.P., Lillehoj, H.S.,  
Matukumalli, L.K. and Van Tassel, C.P.  
TITLE Characterization of expressed sequence tags generated from multiple  
chicken tissues  
JOURNAL Unpublished (2004)  
COMMENT Contact: Christina M. Clover  
Growth Biology Laboratory  
Animal and Natural Resources Institute  
Bldg. 200 Rm215 BARC-East, Beltsville, MD 20705, USA  
Tel: 3015048224  
Fax: 3015048623  
Email: chrisclover@ars.usda.gov  
Single pass sequencing. Bases called and trimmed with phred  
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Best Local Similarity	86.6%; Pred. No. 2e-102;
Matches 505;	Conservative 0; Mismatches 78; Indels 0; Gaps 0;
Qy	647 CCGCTTCACTCTCGCAAGCCACCTGGTTGGTGCAGTCAACCATGAGCCCGAGG 706
Db	1 CAGCCTTCACTCTACGCAATGCCACGTGTTTGTGGTGCAGCTCACGATGAACCCAGAGG 60
Qy	707 TCCACACAGCAACGTGGCTGGTGCAGTGGTGTGACAGCGCCTCAACACTTACTTCCATG 766
Db	61 CCCACGAGACCACTGGTCTGGTGCCTTTGGTCACTGTGCTCAACATTTACTTCCATG 120
Qy	767 TGACCAACTTCTTCTGGATGTTCCGCGAGGGCTGCTACCTGCACACAGCCATCGTGTCA 826
Db	121 TCACCAACTTCTTCTGGATGTTTGGCAGGGCTGCTACCTGCACACAGCCATCGTGTCA 180
Qy	827 CCTACTCCACTGACCGGCTGCGCAATGGATGTTTCATCTGCAITGGCTGGGGTGTGCCCT 886
Db	181 CCTATTCCACCGACAAGCTCCGCAAGTGGATGTTCACTGCAITGGCTGGGTATCCCT 240
Qy	887 TCCCATCATTTGTGGCTTGGGCCAATTTGGGAAGCTGTACTACGACAAATGAGAGTCTGGT 946
Db	241 TTCCATCATTTGTGGCTTGGGCCAATCGGAAGCTGTACTACGACAAATGAGAGTCTGGT 300
Qy	947 TTGCAAAAGCCCTGGGGTGTACACCGACTACATCTACAGGGCCCATGATCTCTGTGCC 1006
Db	301 TTGGGAAGCGAGCAGGAGTTTATCTGACTACATCTATCAAGGTCCCATGATCTCTGTGC 360
Qy	1007 TGCTGTGATCAATTTTCATCTTTCCTTTTCAACATCGTCCGCACTCTCATGACCAAGCTCCGGG 1066
Db	361 TTCTGTATCACTTTCATCTTTCCTTTTCAACATGTTTGGATTTCTATGACCAAGCTCCGAG 420
Qy	1067 CATCAACACGCTGTGAGACCAATTCAGTACAGAAAGGTGTGAAAGCCATCTCTGTGTCTGC 1126
Db	421 CATCAACACGCTGTGAGACCAATTCAGTACAGAAAGCAAGTCAAGGCTACGCTGTGTCTGC 480
Qy	1127 TGCCCCCTCTGGGCATCACTTACATGCTTCTTCTGTCMAATCCCGGGGAGATGAGTCT 1186
Db	481 TGCCCCCTCTGGGGAATCACCTTACATGCTTCTTCTGTCMAATCCCGGGGAGATGAGTCT 540
Qy	1187 CCCGGGTGCTTCTCATCTTCACTTCAACTCTCTTCTGGGAATCCTT 1229
Db	541 CCAGGATGCTTCTTCACTTCACTTCACTTCTTCTGGAGTCTT 583
RESULT 13	
AY406517	
LOCUS	AY406517 1170 bp DNA linear GSS 15-DEC-2003
DEFINITION	Mus musculus CRHR2 gene, VIRTUAL TRANSCRIPT, partial sequence,
ACCESSION	AY406517
VERSION	AY406517.1
KEYWORDS	GSS.
SOURCE	Mus musculus (house mouse)
ORGANISM	Mus musculus
	Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;



Query Match	27.7%; Score 438.2; DB 8; Length 766;
Best Local Similarity	79.1%; Pred. No. 1.9e-97;
Matches 521; Conservative	0; Mismatches 138; Indels 0; Gaps 0;
QY	787 TTTCGGCGAGGCTGTACCTGCACACAGCCATCGTGTCTCACTTACTCCACTGACCGGCTG 846
DB	
QY	1 TTTCGGCGAGGCTGTACCTGCACACAGCGCTATTGTGCTAACTTACTGCAGCGCAAACTG 60
DB	
QY	847 CGCAAAATGGATGTTTCATCTGTCATTGGCTGGGGGTGCGCTTCCCTCCCAATCATTTGTGGCCTGG 906
DB	
QY	61 CGCAAAATGGATGTTTCATCTGTCATCGGCTGGTGTTATCCCTTCCCATCATTTGTGGCTTTG 120
DB	
QY	907 GCCATTGGGAAGCTGTACTACGACAAATGAAAGTGTGGTTGGCGAAAGGCTGGGGGTG 966
DB	
QY	121 GCCATTGGCGAACTTTACTATGACATGAAAGTGTGGTTGGTAGAAAGCAGAGATC 180
DB	
QY	967 TACACCGACTACATCTACACGGGCGCCCATGATCTGTCTGTCTGTGATCAATTTTCATCTTC 1026
DB	
QY	181 TACACAGATTTTATCTACCGAGGACGGTTATCTTGTACTGTCTGATCACTTTTATTTT 240
DB	
QY	1027 CTTTTTCAACATCGTCGCGATCTCATGACCAAGCTCGGGCATCCACCAAGCTCTGAGACC 1086
DB	
QY	241 TTATTCAACATAGTGCAGATTCTGATGACAAAGCTCCGAGCTTCCACCATTCAGAGACC 300
DB	
QY	1087 ATTTCAGTACGGAAGGCTGTGAAAGGCACTCTCTGGTGTGTGCCCCCTCTCTGGGCAATCACC 1146
DB	

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